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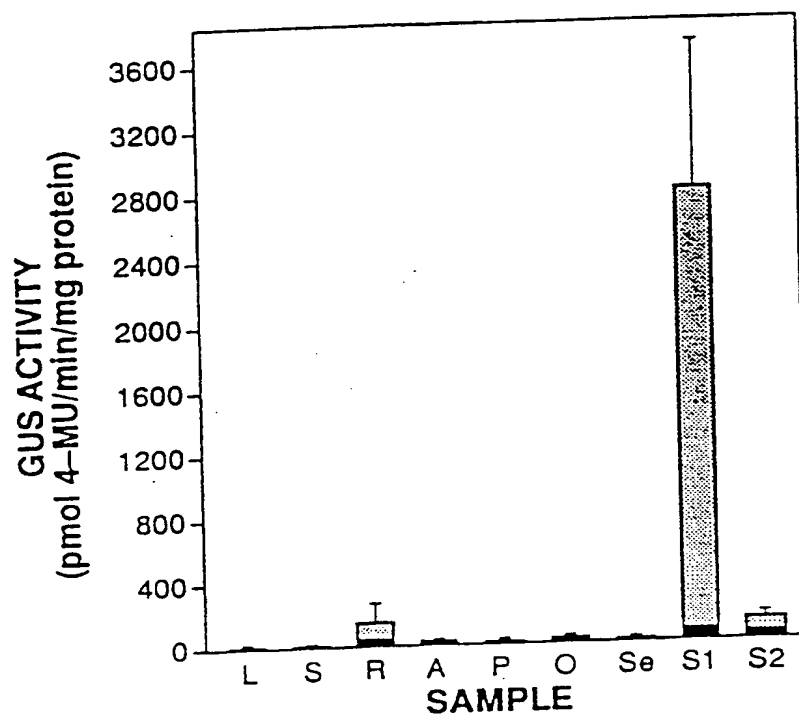


FIGURE 1

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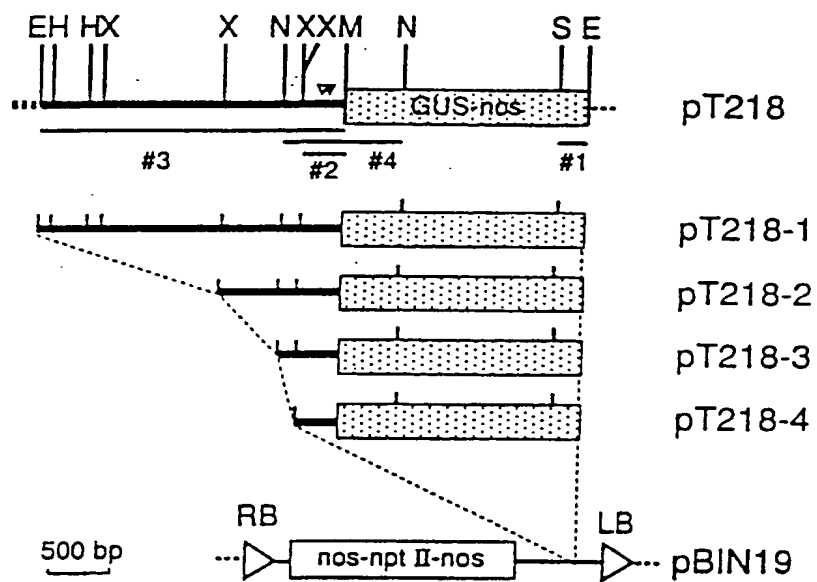


FIGURE 2

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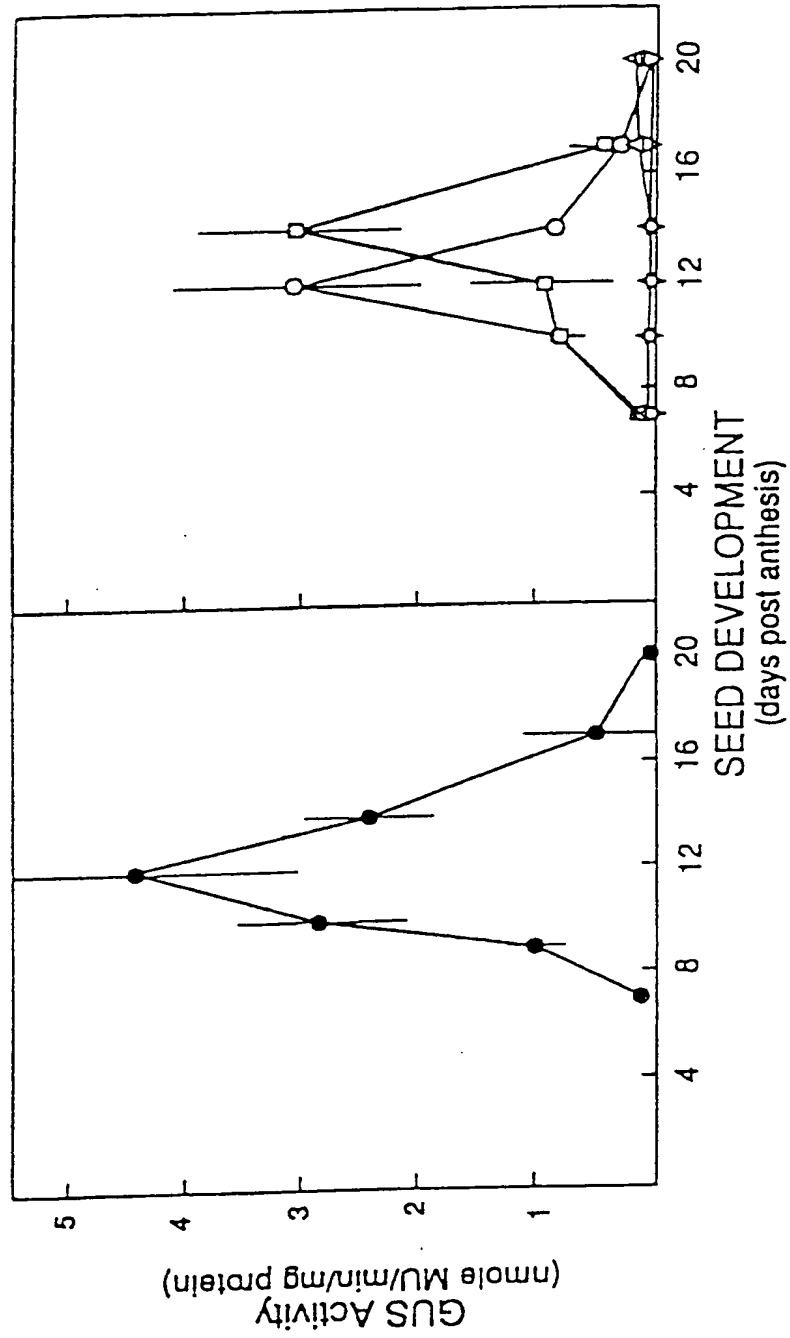


FIG. 3A

FIG. 3B

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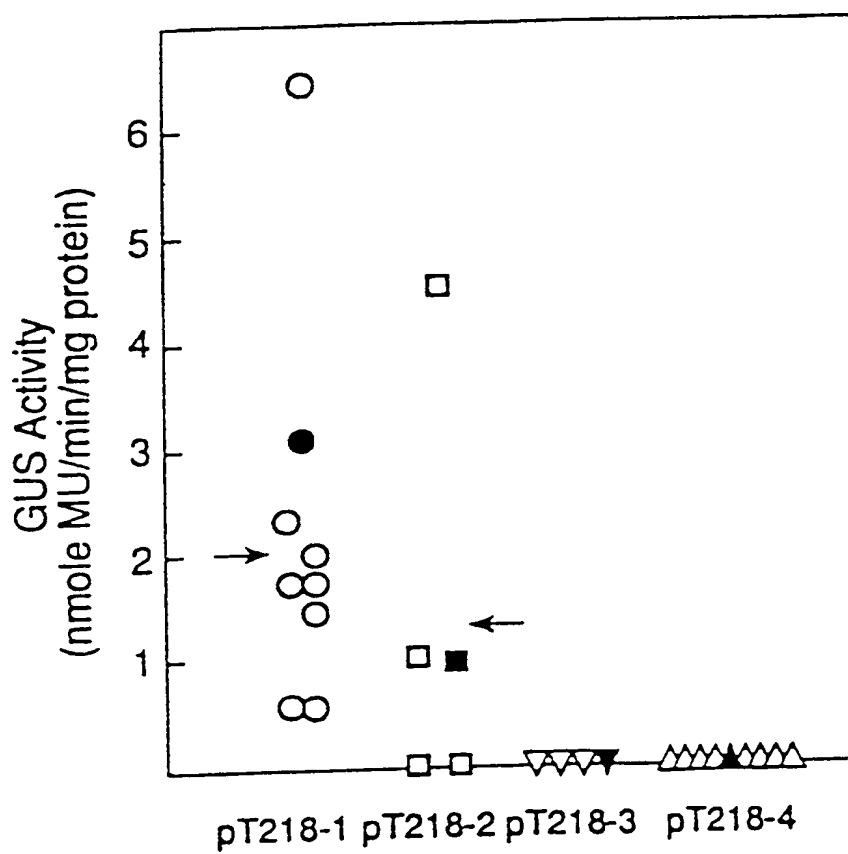


FIGURE 4

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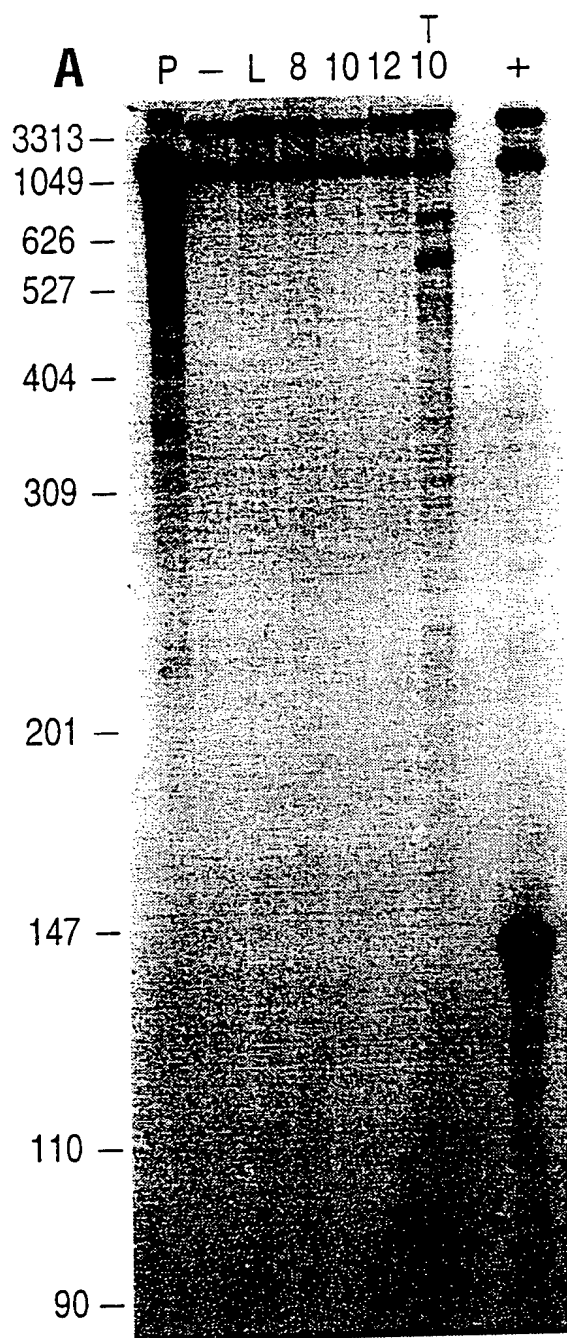


FIG. 5A

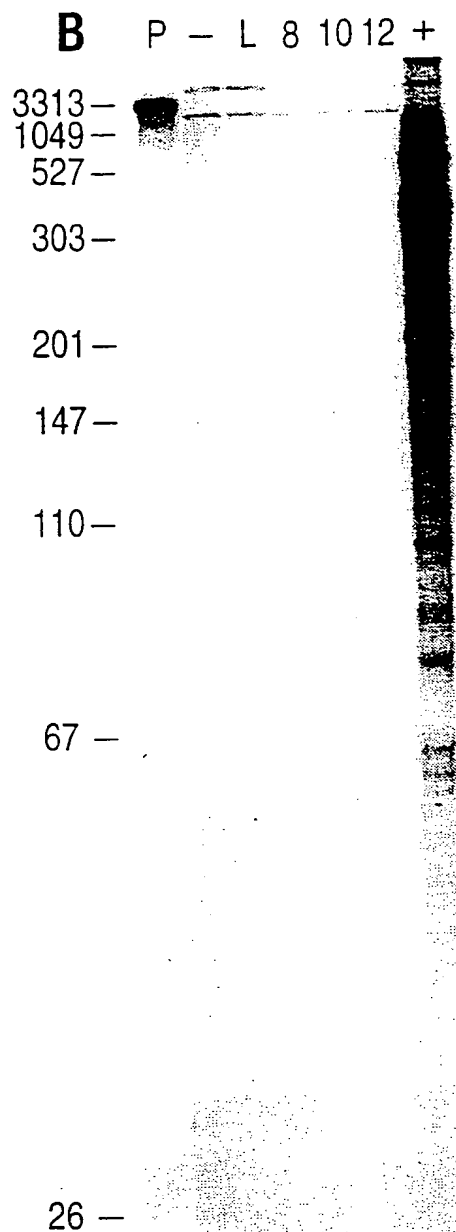


FIG. 5B

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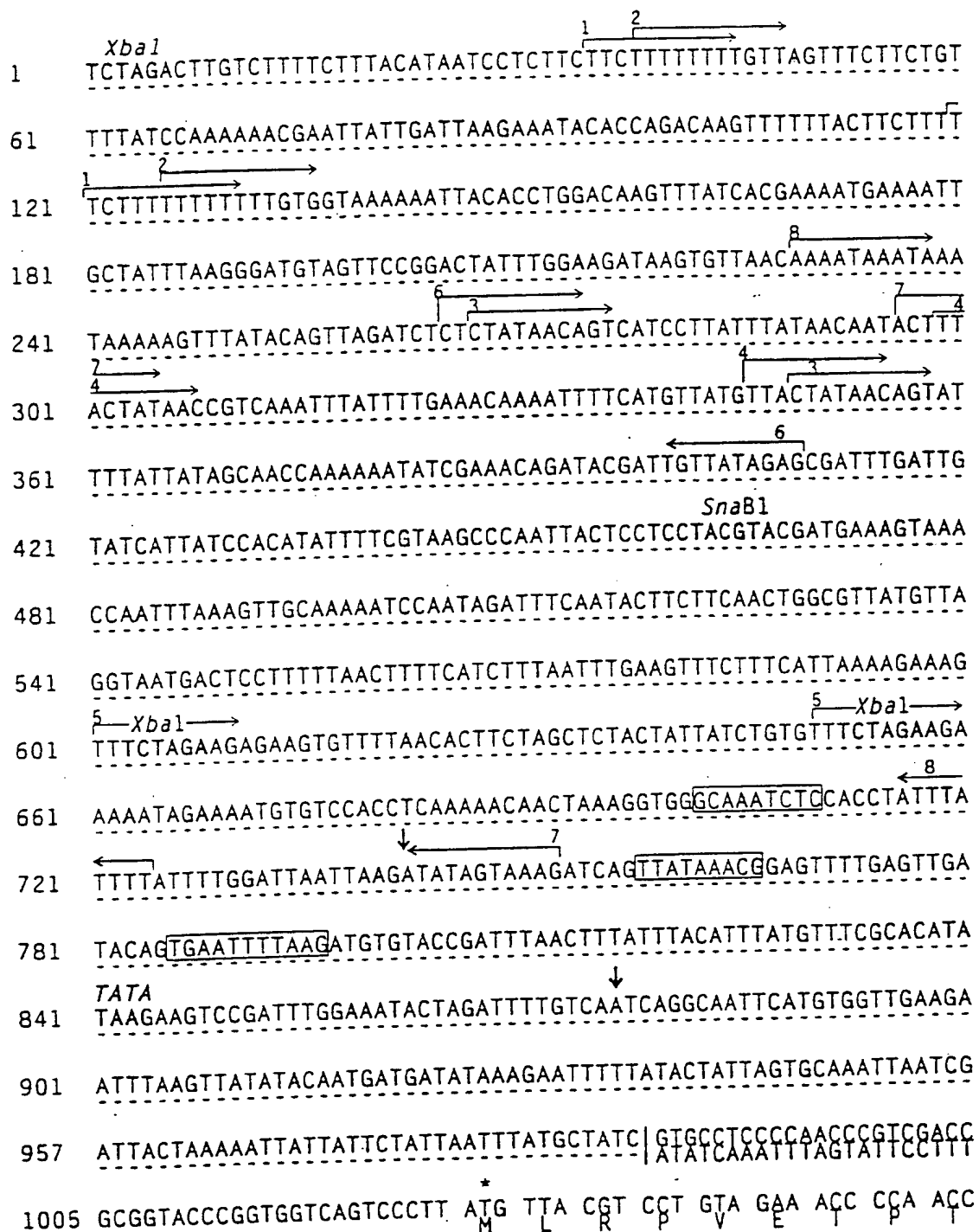
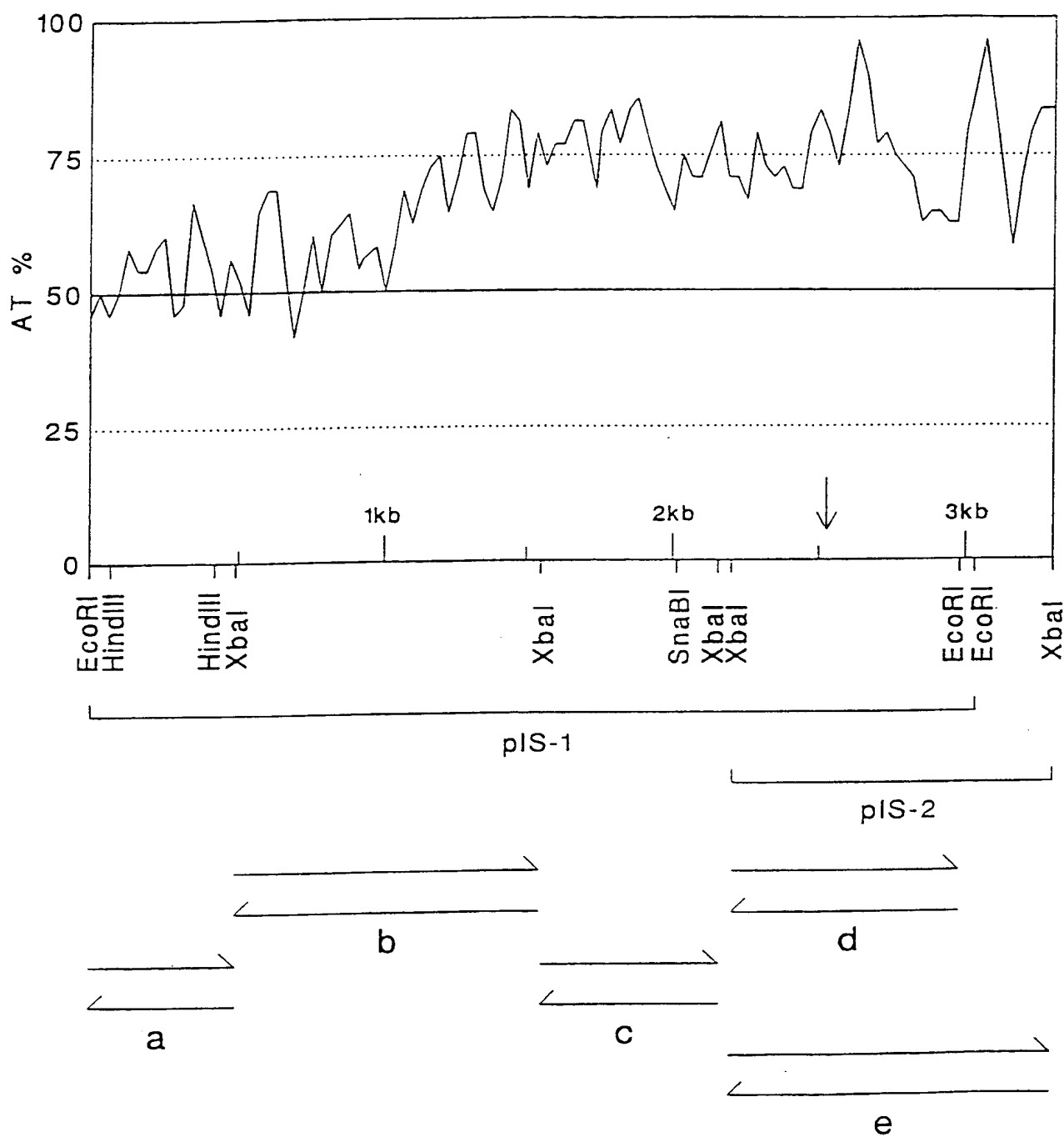


FIGURE 6

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**FIGURE 7**

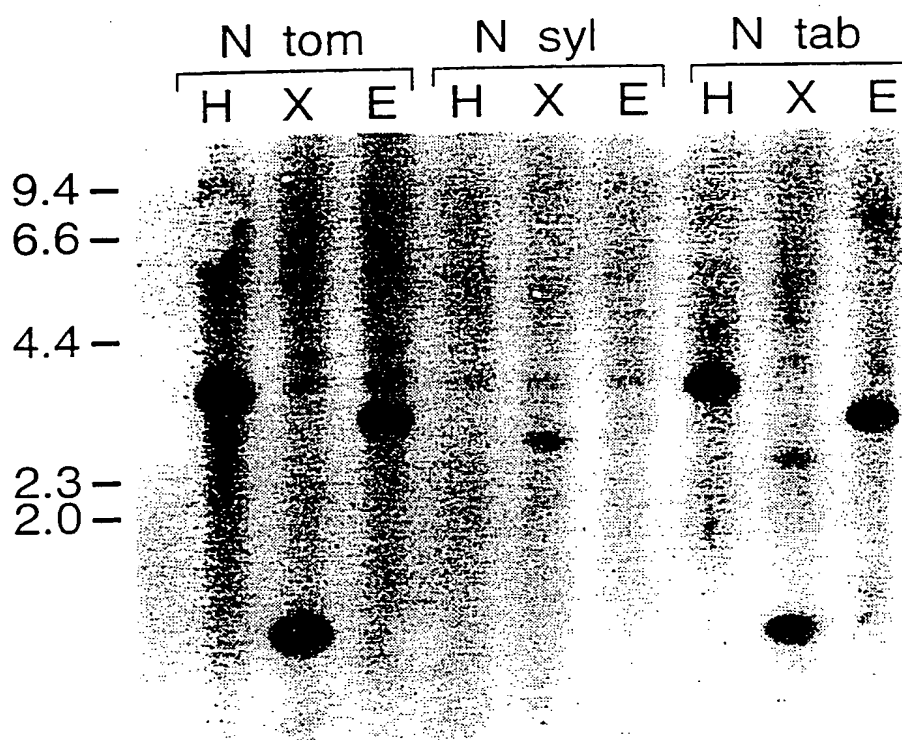


FIG. 8



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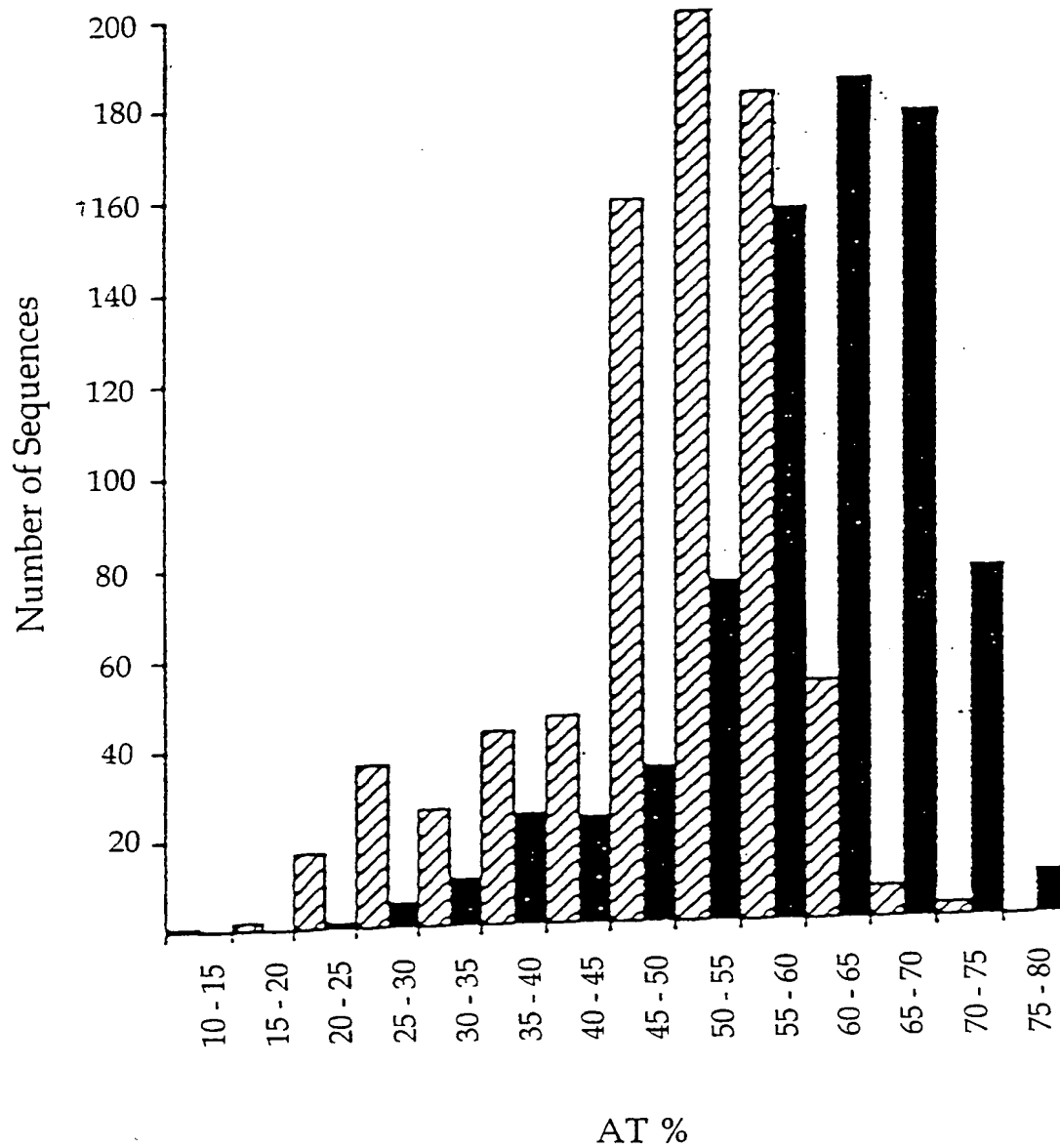


FIGURE 9

SEED COAT  
EMBRYO  
STEM  
ROOT  
LEAF  
POD  
FLOWER



FIG. 10D

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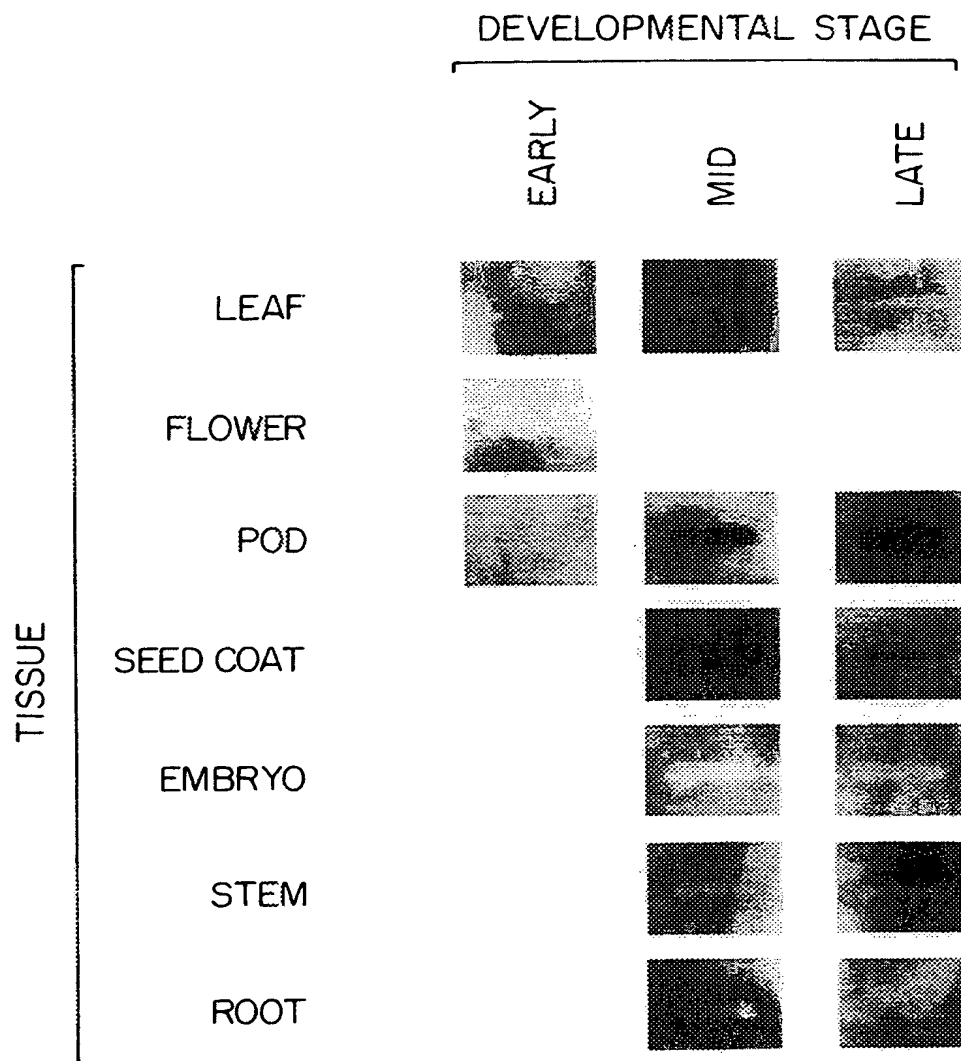


FIG. 10E

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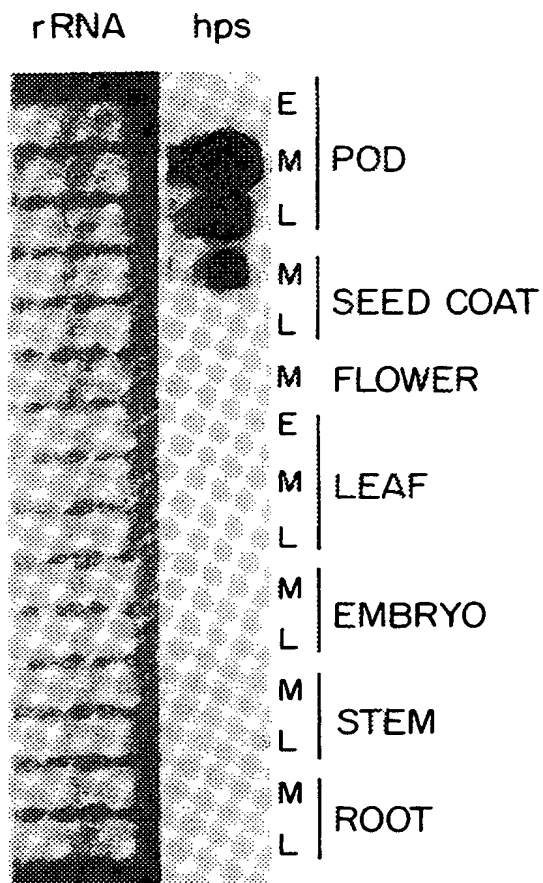


FIG. IOF

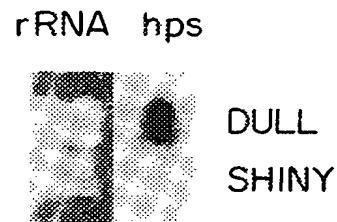


FIG. IOG

FO8220" EEE/960

RESTRICTION MAP OF SC20

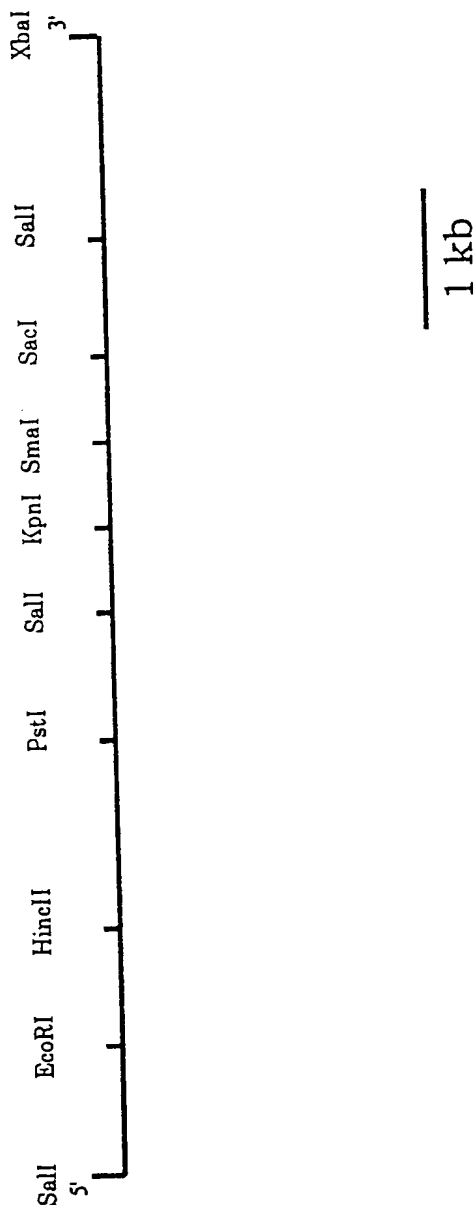
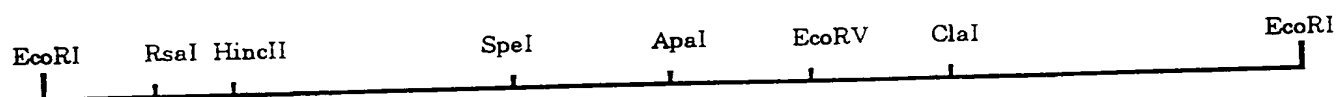


FIGURE 11(A)

## RESTRICTION MAP OF SC21



1 kb

*FIGURE 11(B)*

- ☐ BamH I - Restriction Map (1 cut)
- ☐ Bgl II - Restriction Map (1 cut)
- ☐ Hind III - Restriction Map (1 cut)
- ☐ Xba I - Restriction Map (4 cuts)

☐ Hps Open Reading Frame:

☐ TATA-BOX(1) - Signals

☐ Coverage - Direct Repeats

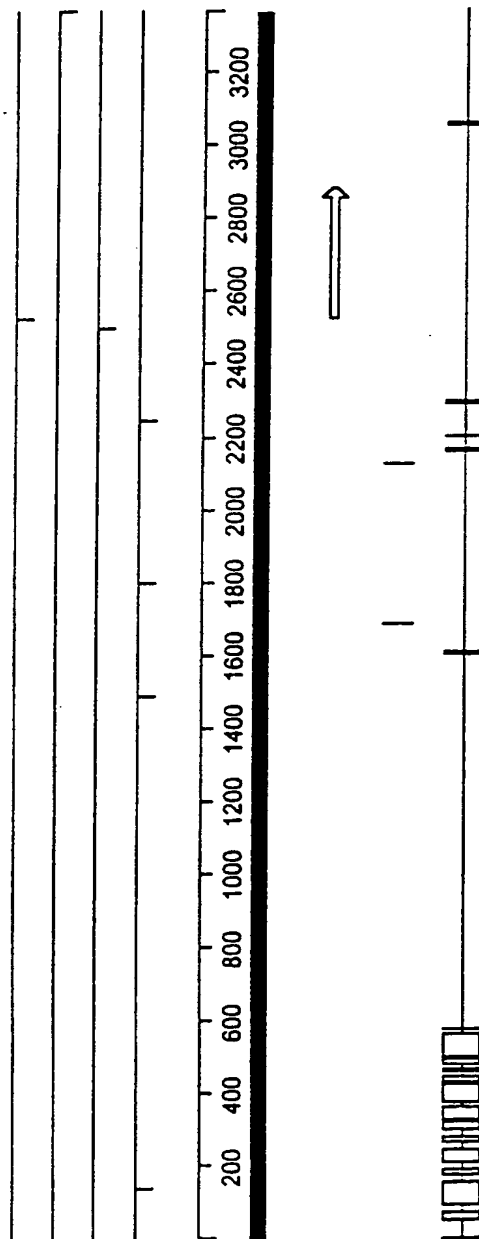
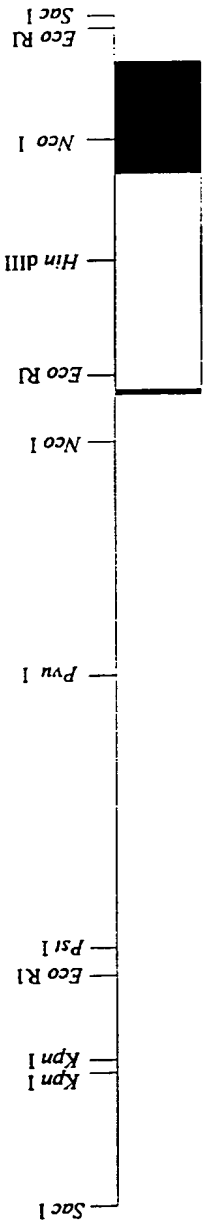


FIGURE 11(C)



Restriction map of *sc4*

The shaded and open boxes represent exons and introns respectively.

FIG. 11(D)



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6 DAF

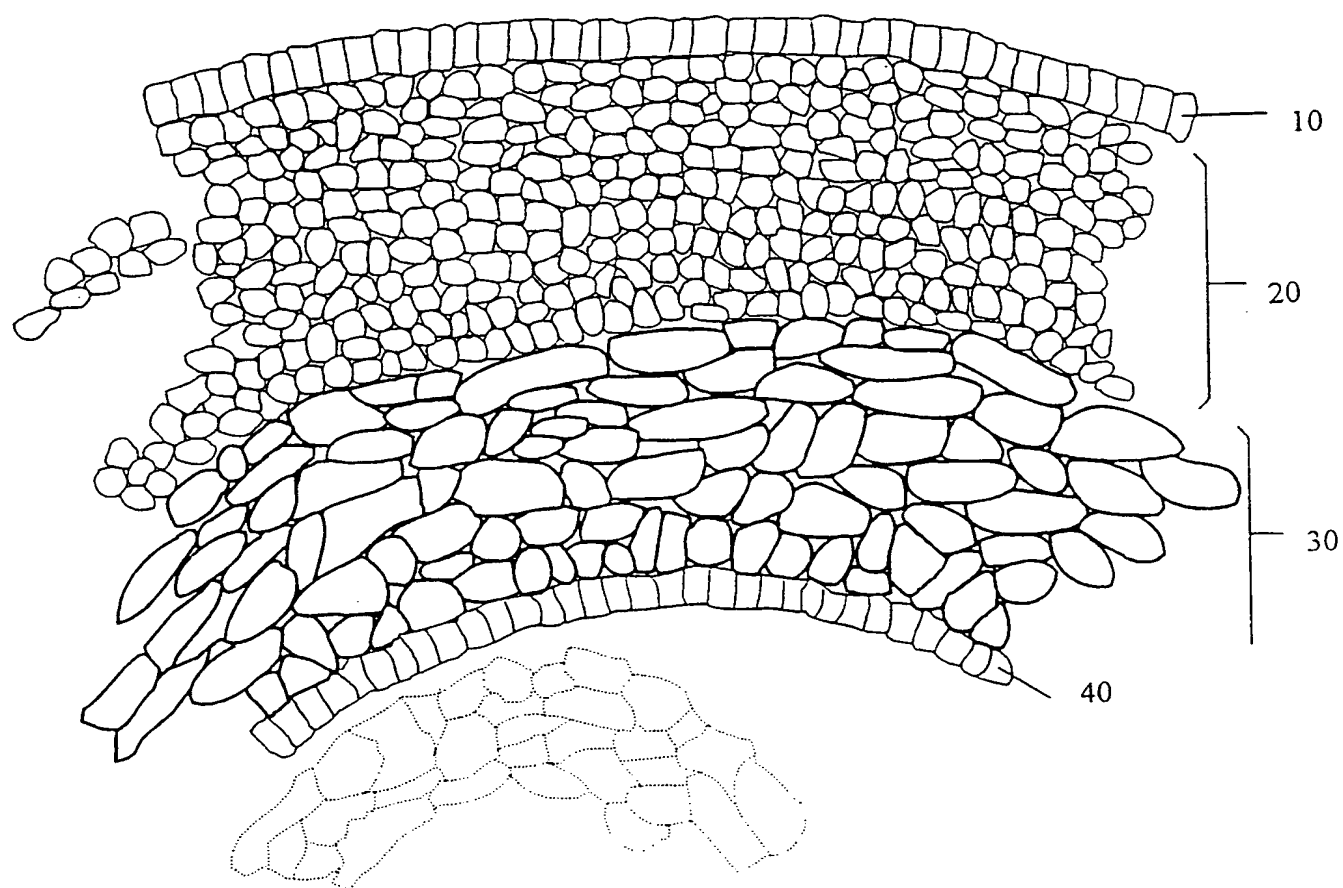


FIGURE 12(a)

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12 DAF

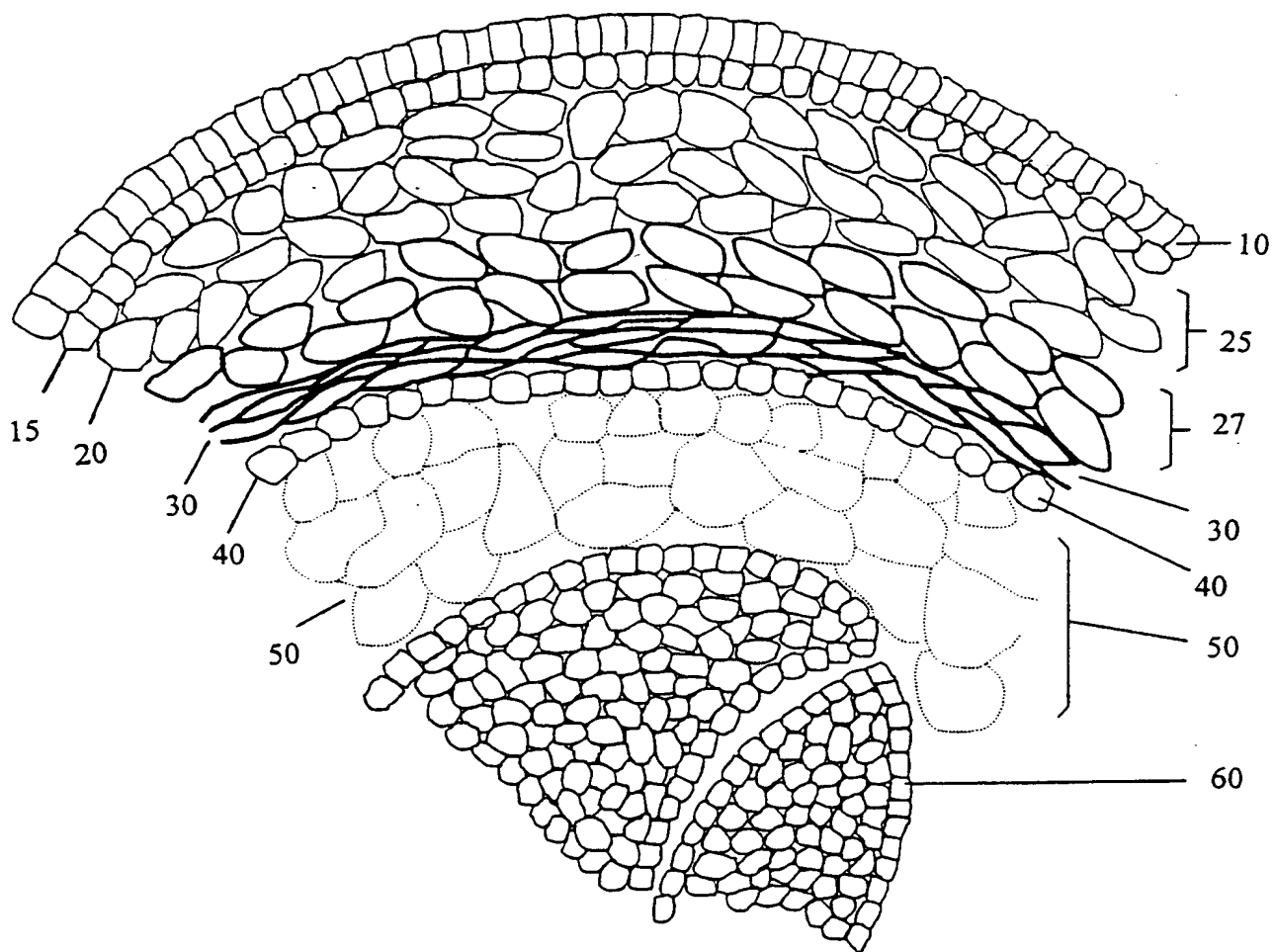


FIGURE 12(b)

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18 DAF

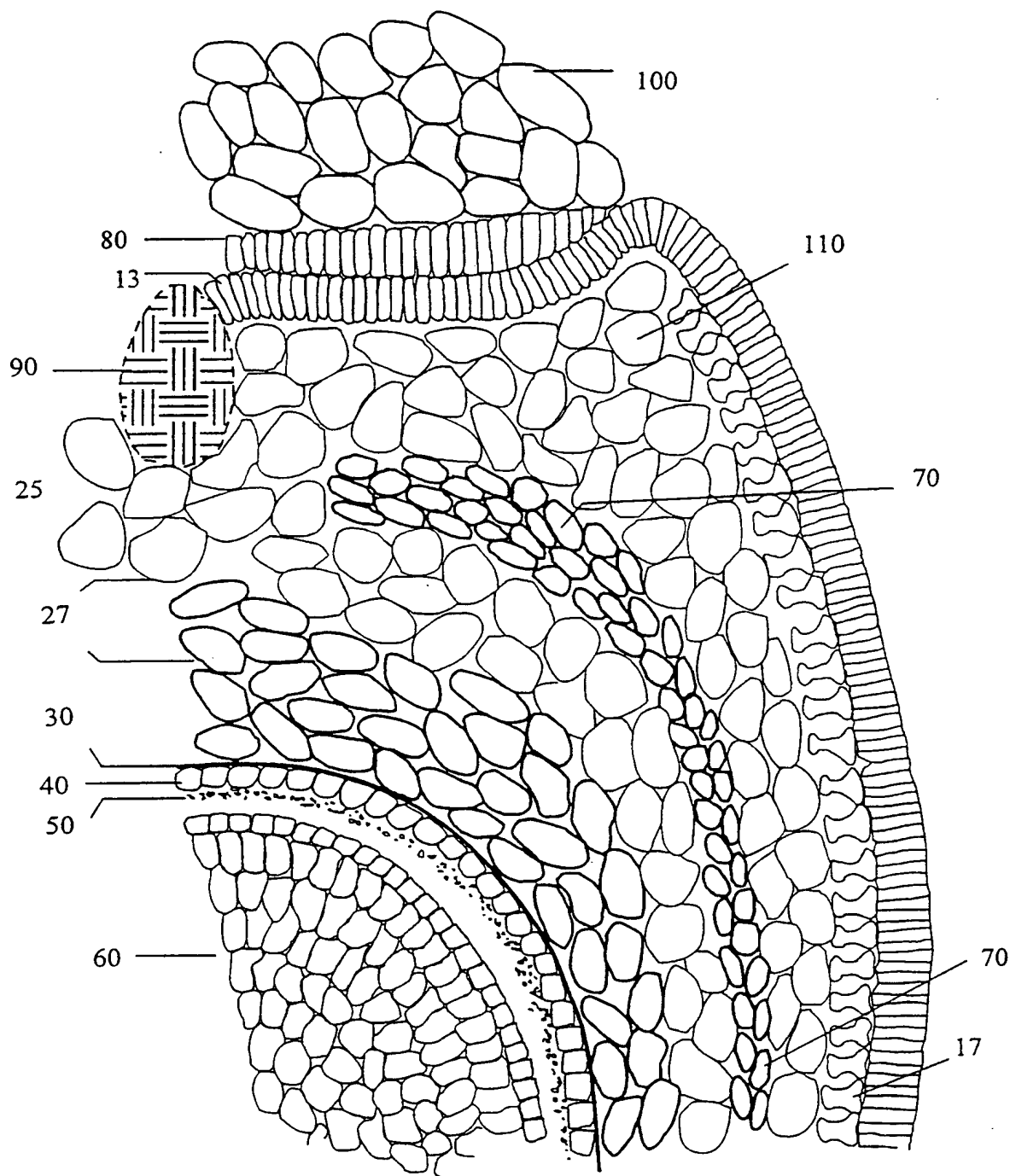


FIGURE 12(c)

FIG. 13A

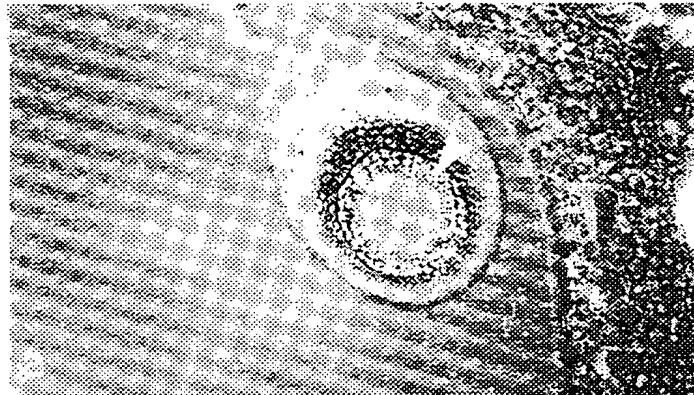


FIG. 13B

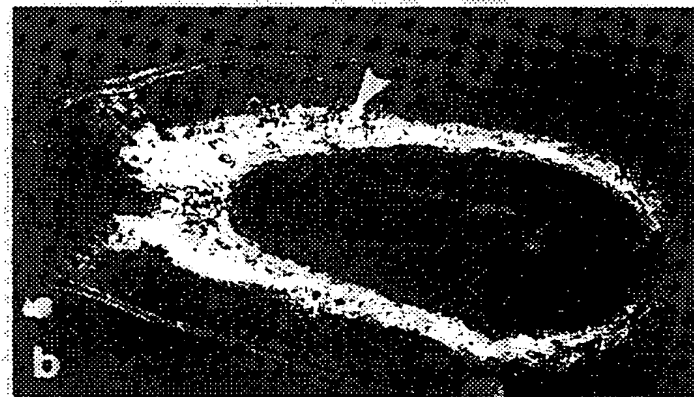
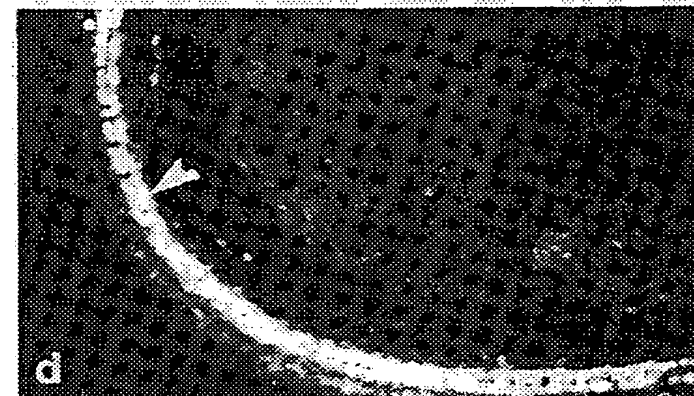


FIG. 13C



FIG. 13D



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FIG. 13E

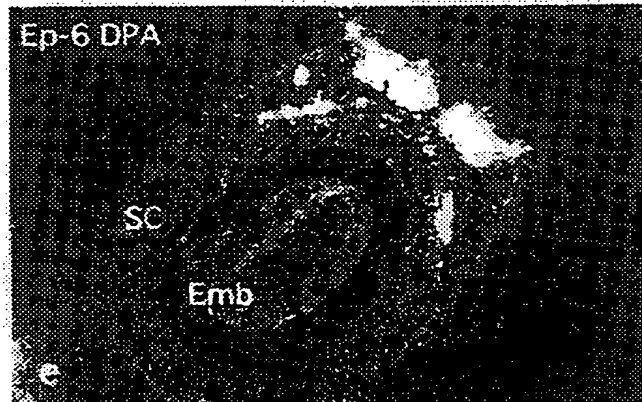


FIG. 13F

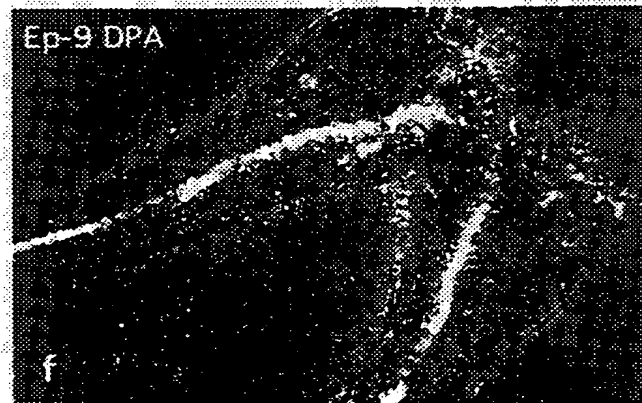
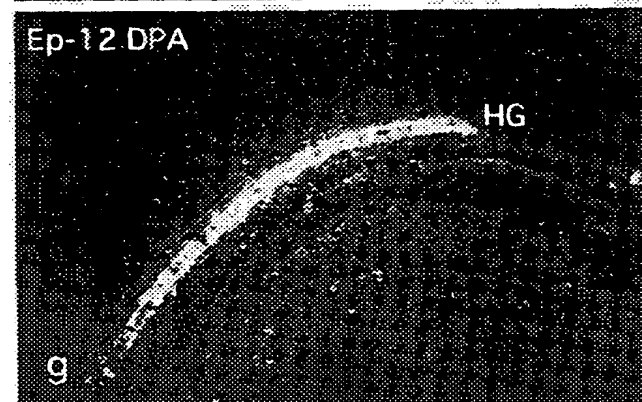


FIG. 13G



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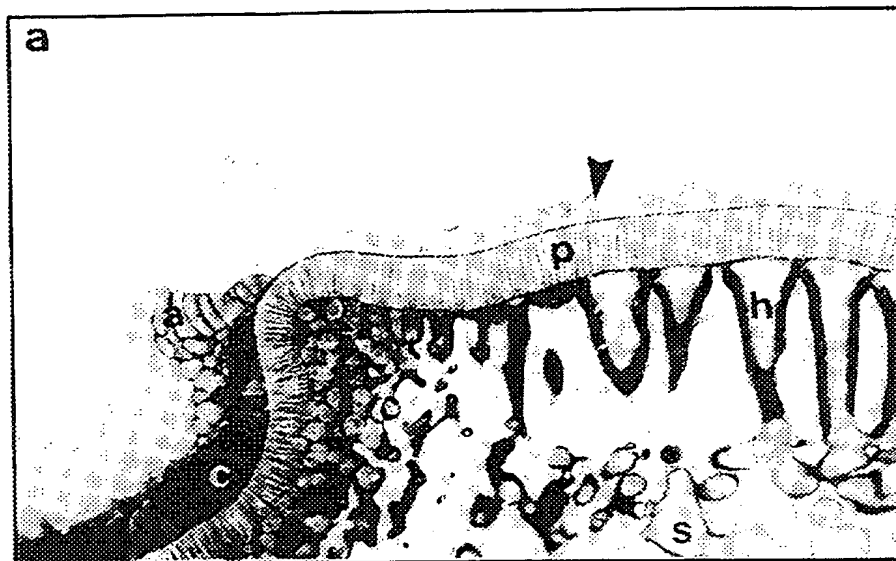


FIG. 14A

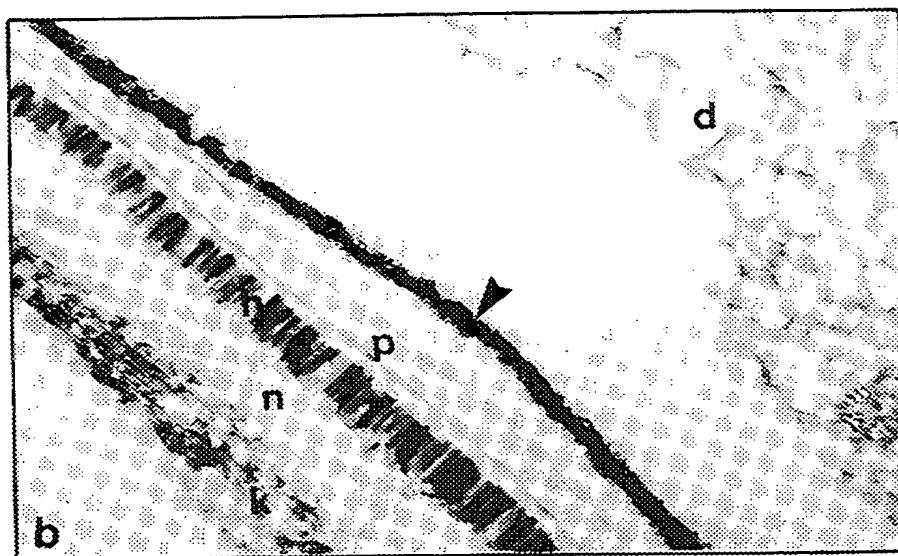


FIG. 14B

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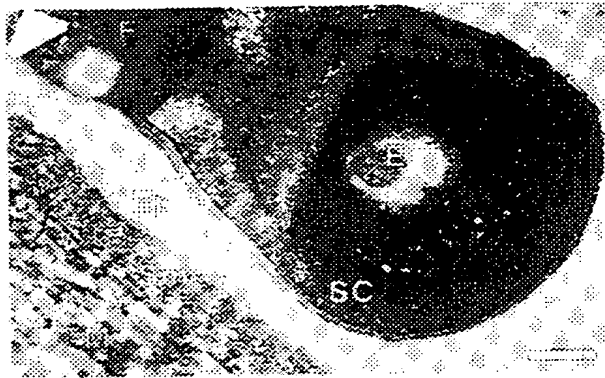


FIG. 14C

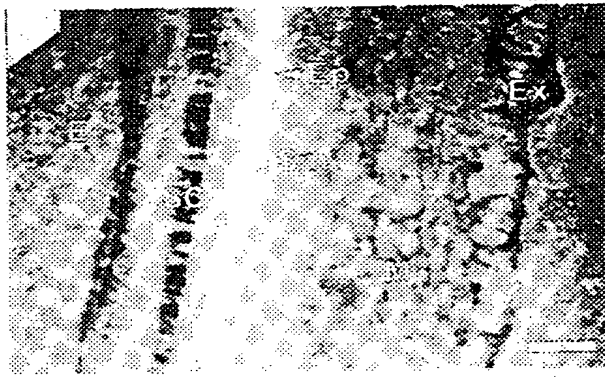


FIG. 14D

09673333 02220 00220

TAAGCTTTCAAGAGACAAACTGCTTTGAAAAATGGGATCCAAAGTTGTTGCATCCGTTGC	50
<u>M G S K V V A S V A</u>	10
CCTTCTCCTCTCCATCAACATTCTTTTCATTTCATGTTAGCTCCAGCAGCCACTACGA	120
<u>L L L S I N I L F I S M V S S S S H Y D</u>	30
TCCACAGCCCCAACCTTCTCAGGTCACTGCTCTTATTACACGACCTAGTTGTCCGGATCT	180
<u>P Q P Q P S H V T A L I T R P S C P D L</u>	50
GAGTATTTGCCTCAATATTTTAGGCGGGTCTCTAGGAACCGTGGATGATTGTTGTGCCCT	240
<u>S I C L N I L G G S L G T V D D C C A L</u>	70
CATCGGTGGTCTTGGTGACATTGAAGCCATTGTGTGCCCTTGCATCCAACCTCAGGGCCCT	300
<u>I G G L G D I E A I V C L C I Q L R A L</u>	90
CGGAATATTAAACCTTAACCGTAATTTGCAGTTAATATTAAACTCCTGTGGACGAAGCTA	360
<u>G I L N L N R N L Q L I L N S C G R S Y</u>	110
CCCGTCAAACGCCACTTGCCCCCGAACCTAAGAACAGAATATGTATGGCACTAATTACCA	420
<u>P S N A T C P R T *</u>	119
TATTACTTCGTATCATGGTGTGTTGTTTGTTGTCTGTGTTTAAAGTTAAGGATGTTATAC	480
CCTTCGTGCCTGCTACATATATATAGTGGGCACTATAATATTACCAATAAATTAAACGTCC	540
ATATATAAGAATAATAATAAATAAATAATTTCTATACAAATAAAGGTTACGTAATGT	600
TGTTGTTCTCGTGGATGGGGATCTTATCTTCTCCTCGCTATCTTTGTTTATCGTATTTCT	660
AGTGAAAGTTGTTCAATAAAAGTCCTTTGTTCAACAAGT (A) <sub>n</sub>	700



MGSKVVASVALLLSINILFISMVSS 25  
SSHYPQPPSHVTA<sup>1</sup>ITRPSCPD<sup>2</sup>L 50  
SICLNILGGS<sup>3</sup>SLGTVDCCALIGGLG 75  
DIEAIVCLCIQLRALGILNLNRNLQ 100  
LILNSCGRSYPSNATCPRT 119

FIG. 15(B)

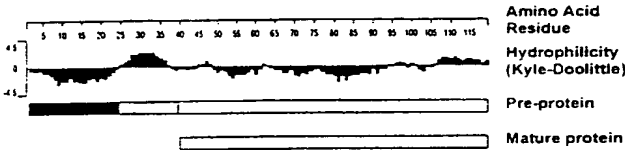


FIG. 15(C)

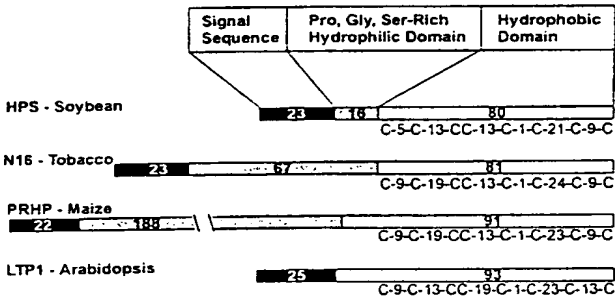


FIG. 15(D)

FIG. 15

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CULTIVAR: CLARK  
PHENOTYPE: DULL

WILLIAMS 82  
SHINY

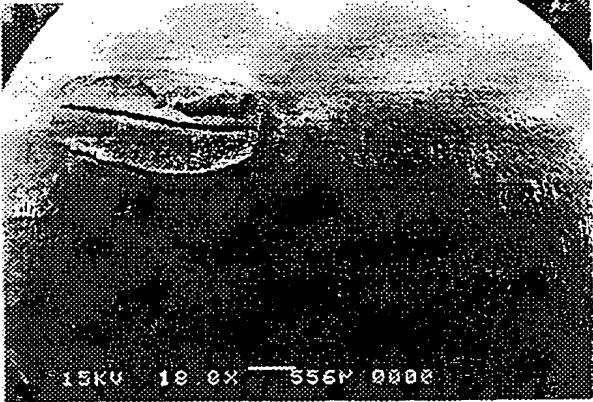
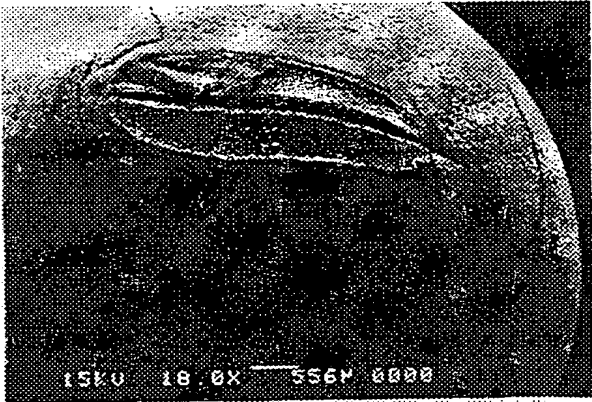


FIG. 16A

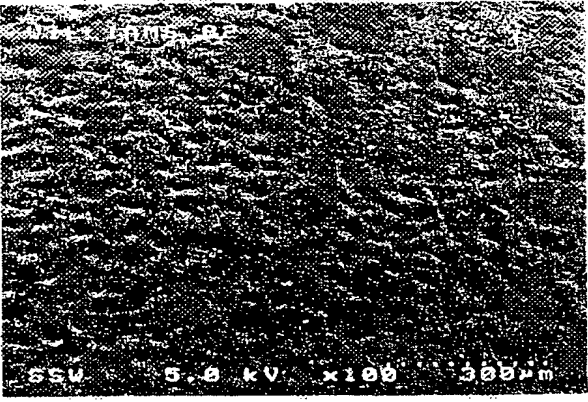
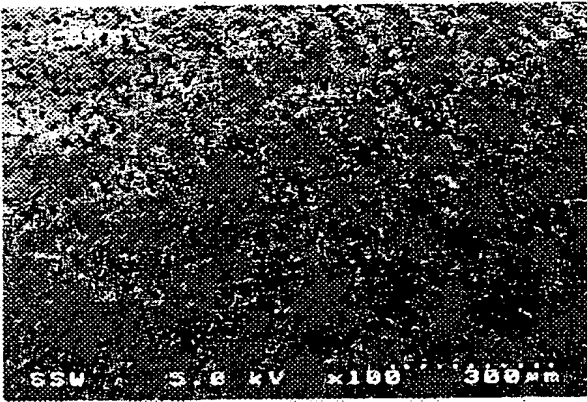


FIG. 16B

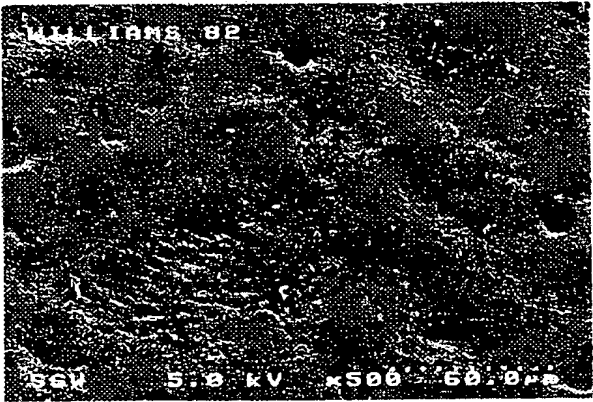


FIG. 16C

09673333-02801

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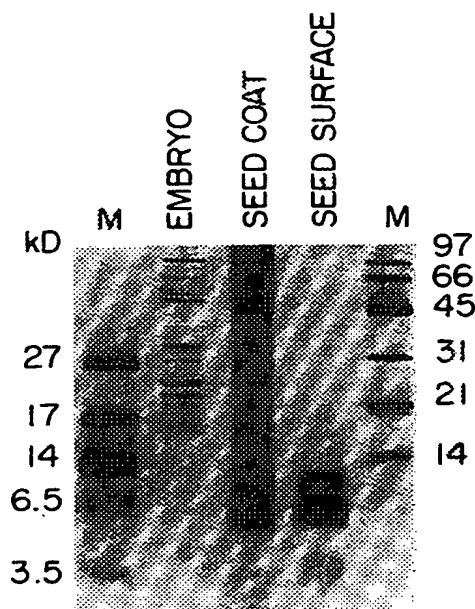


FIG. 17A

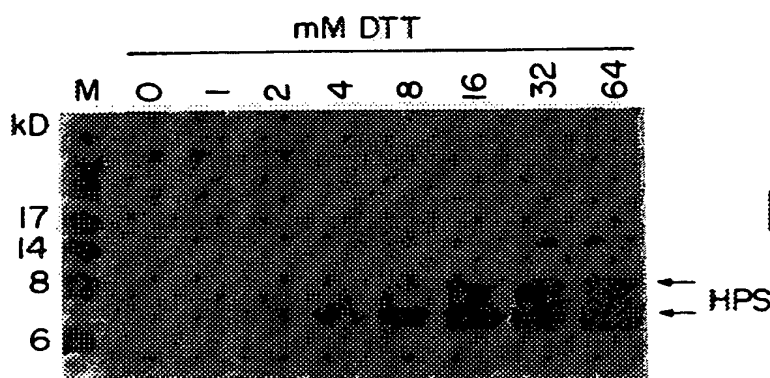


FIG. 17B

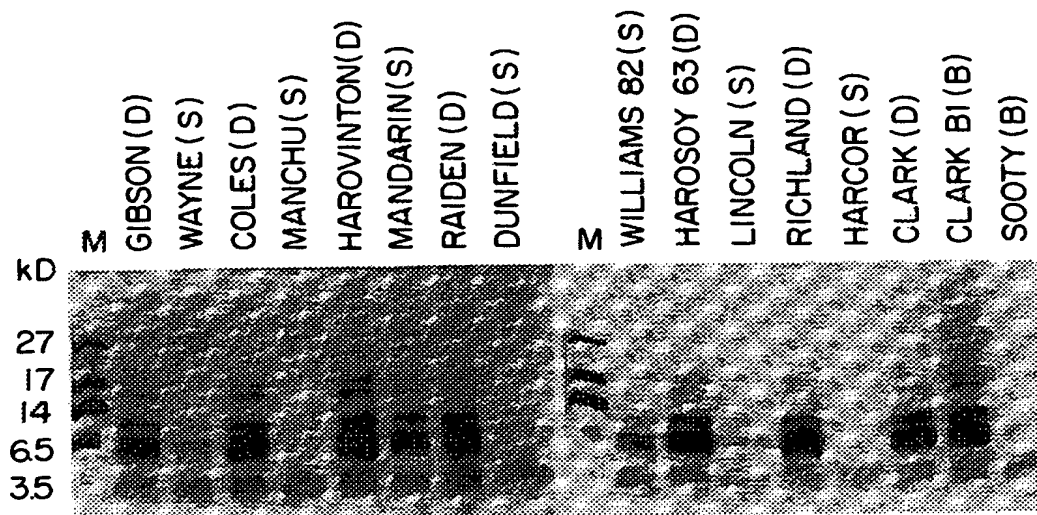


FIG. 17C

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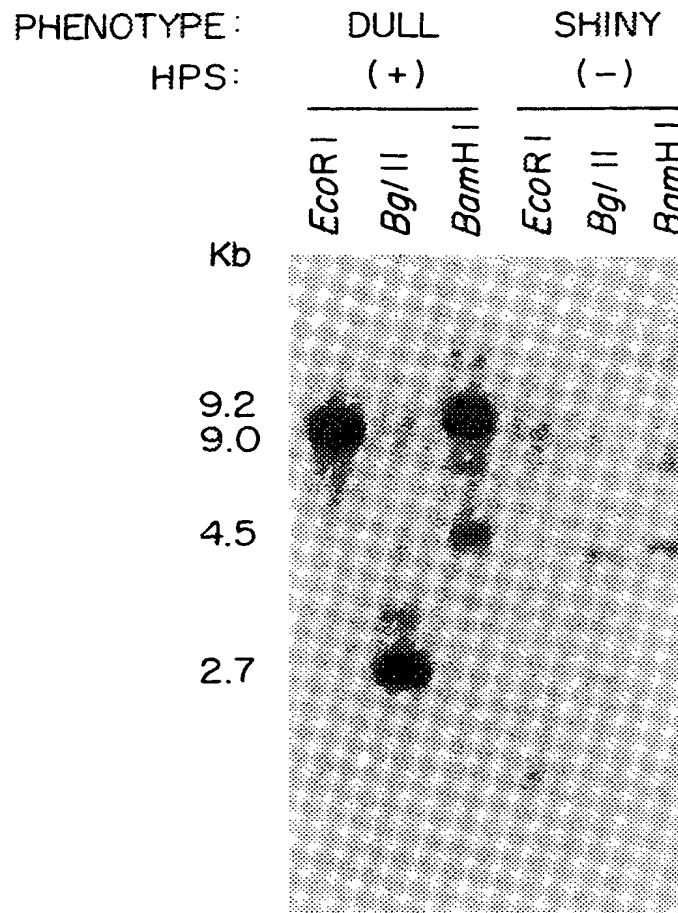


FIG. 18



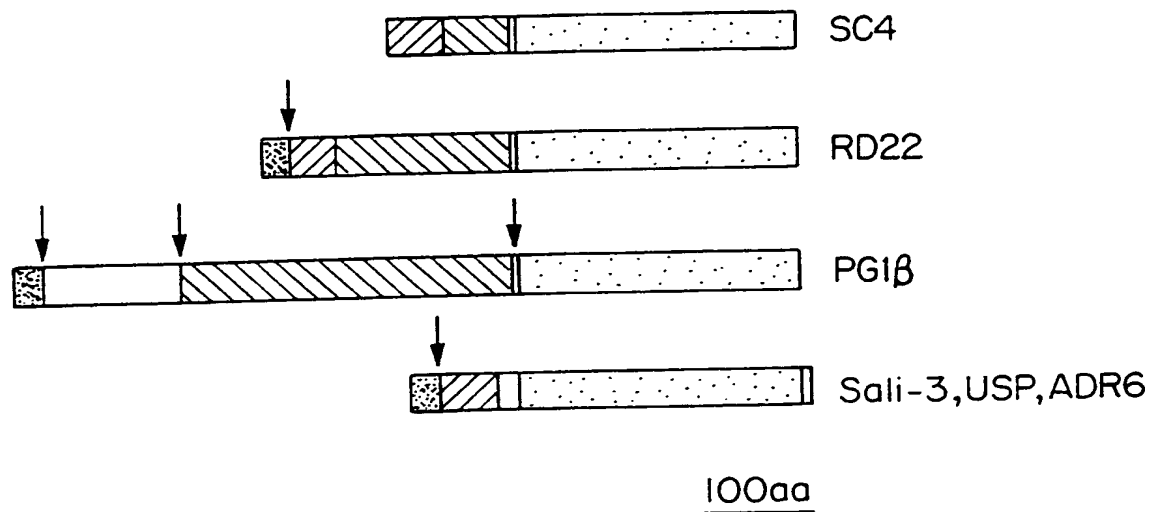

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## A

SC4c	FFLEEDLRAG	KIFNMKFVNN	--TKATVPLL	PRQISKQIPF	SEDKKKQVLA	MLGVEANSSN	131
RD22	FFLEKDLVRG	KEMNVRFNAE	DGYGGKTAFL	PRGEAETVPF	GSEKFSETLK	RFSVEAGSEE	235
PG1B	FFREKMLKSG	TIMPMPDIK-	-DKMPKRSFL	PRVIASKLPF	STSKIAELKK	IFHAGDESQV	472
Sali3-2	FFYKEDLHPG	KTMKVQFTKR	-----	-----PY	AQPY--GVYT	WLTDIKDTSK	215
USP	FF-EHDLHPG	KNFNLGHTNS	VGSIIR----	-----PF	TKSR--QGV	--DSIWLANK	111
ADR6	FFYKEDLHPG	KTMKVQFSKP	-----	-----PF	QQPW--GVGT	WLKEIKDTTK	111
SC4c	AKIIAETIGL	CQE-PATEGE	RKHCATSLES	MVDFVVSALG	KN-VGAFSTE	KERETESGK-	188
RD22	AEMMKKTIEE	C-EARKVSGE	EKYCATSLES	MVDFS VSKLG	KYHVRAVSTE	VAKKNAPMQK	294
PG1B	EKMIGDALSE	C-ERAPSAGE	TKRCVNSAED	MIDFATSVLG	RN-VVVRTTE	DTKGSNGNIM	530
Sali3-2	EGYSFEEI--	CIKKEAFEGE	EKFCAKSLGT	VIGFAISKLG	KN-IQVLSSS	FVNKQE----	168
USP	EKQSLEDF--	CYSPTAI-AE	HKHC VSSLKS	MIDQVISHFG	STKIKAISSN	FAPYQD----	164
ADR6	EGYSFEEL--	CIKKEAIEGE	EKFCAKSLGT	VIGFAISKLG	KN-IQVLSSS	FVNKQD----	164
SC4c	FVVVKNVGRK	LGDDKVIACH	PMSYPYVVF	CHLVPR-SSG	YLVRLKGEDG	VR-VKAVVAC	246
RD22	YKIAAAGVKK	LSDDKSVVCH	KQKYPFAVY	CHKAMM-TTV	YAVPLEGENG	MR-AKAVAVC	352
PG1B	I-GSVKGING	GKVTKSVSCH	QTLYPYLLYY	CHSVPKVRVY	EADILDPNK	VKINHGVAIC	589
Sali3-2	-QYTVEGVQN	LG-DKAVMCH	GLNFRTAVFY	CHKV-RETTA	FVVPLVAGDG	TK-TQALAVC	224
USP	-QYVVEDVKK	VG-DNAV MCH	RLNFEKVVEN	CHQV-RDTTA	YVVS LVASDG	TK-TKALTVC	220
ADR6	-QYTVEGVQN	LG-DKAVMCH	RLNFRTAVFY	CHEV-RETTA	FMVPLVAGDG	TK-TQALAIC	220
SC4c	HRDTSKWDHN	HGAFKVLNLK	PGNGTVCHVF	TEGNLLWLPN	*		286
RD22	HKNTSAWNP	HLAFKVLKVK	PGTVPVCHFL	PETHVVWFSY	*		392
PG1B	HVDTSWGP	HGAFVALGSG	PGKIEVCHWI	FENDMTWAIA	D*		630
Sali3-2	HSDTSGMNH-	HILHELMGVD	PGTNPVCHFL	GSKAILWVPN	ISMDTAYQTN	VV* 276	
USP	HHDTTRGMNP-	ELLYEAEV	PGTVPVCHFI	GNKAAAWVPN	HTADNLCVM*		268
ADR6	HSNTSGMNH-	QMLHQLMGVD	PGTNPVCHFL	GSKAILWVPN	LSVDTAYQTN	IVA* 272	
<b>B</b>							
SC4c	--NAALTPRL	YWETMLPRTP	LPKAITELLS	L	29		
RD22	AIAADLTPER	YWSTALPNT	IPNSLHNL	F	48		
Sali3-2	HVHASLPEED	YWEAVWPNT	IPALRDVLK	P	53		
USP	GITATSSGED	YWQSIWPNT	LPKTFSDLLI	P	48		
ADR6	ARESHARDED	FWHAVWPNT	IPSSLRDLLK	P	49		

FIG. 19(B)

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HYDROPHOBIC REGION: CONSERVED SEGMENT: REPEATED REGION: BURP DOMAIN: 

PEPTIDE CLEAVAGE POINT: ↓

FIG. 19C

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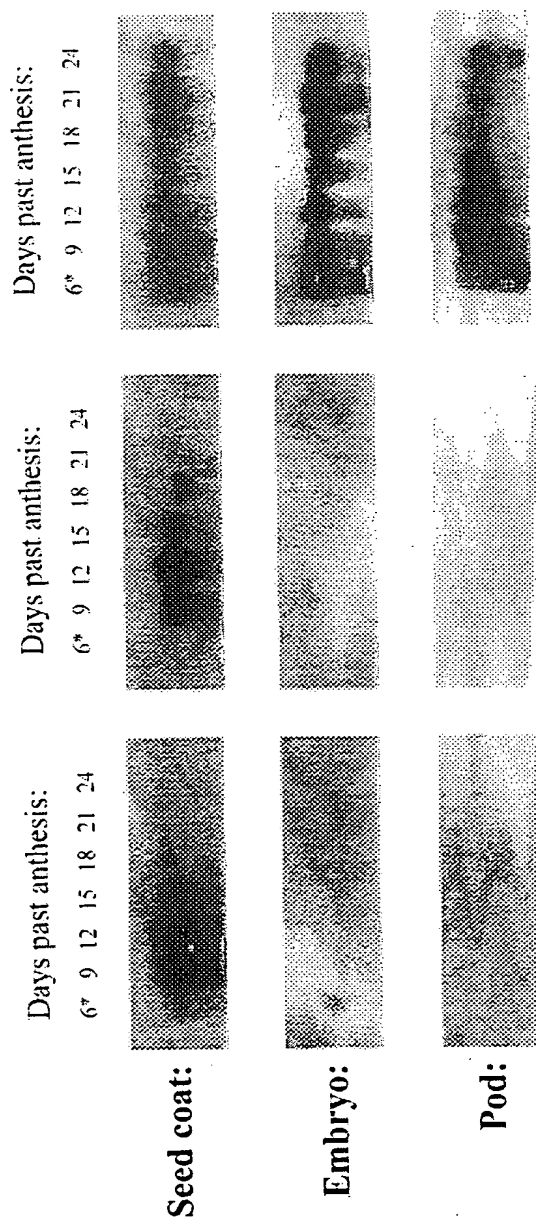


Fig. 20 C

Fig. 20 B

Fig. 20 A



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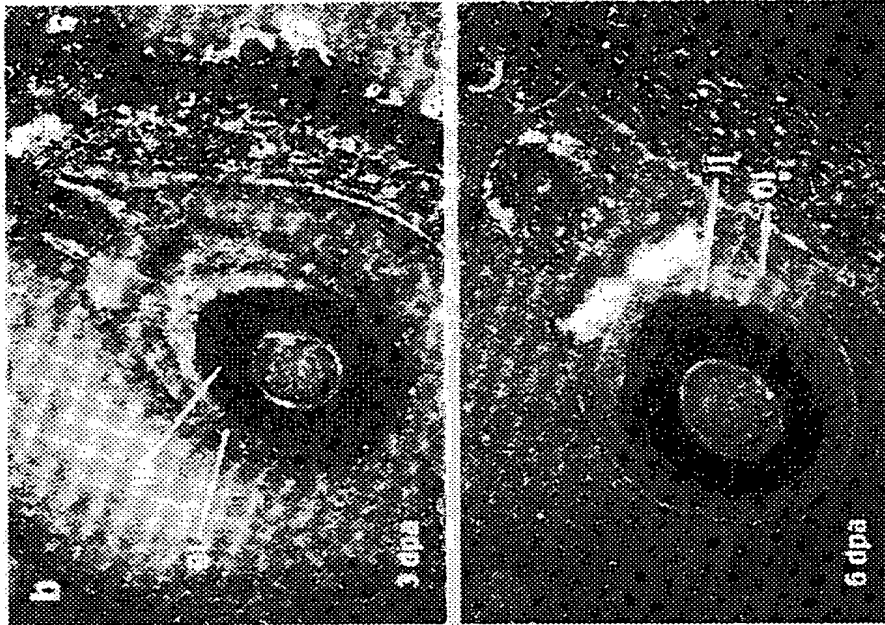


FIG. 2IB

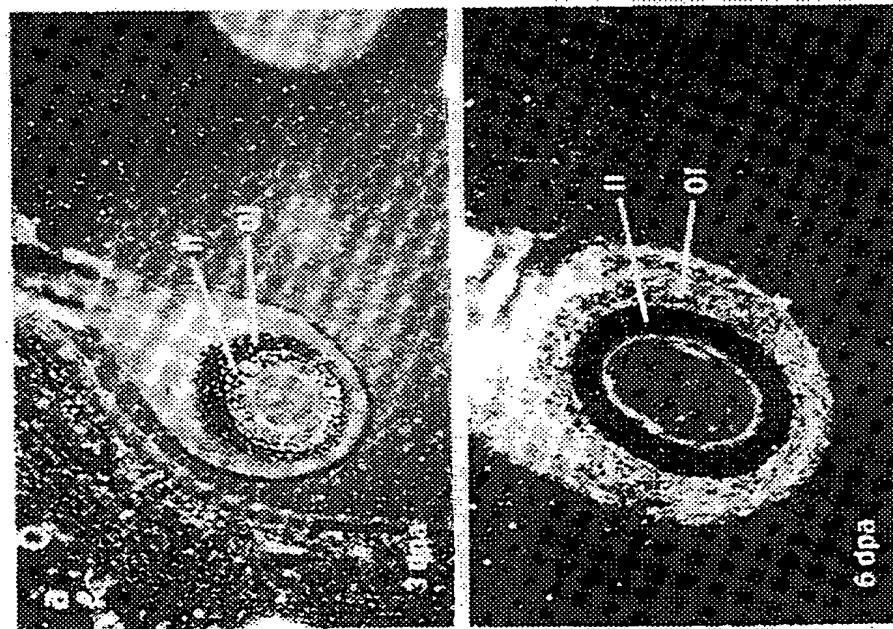


FIG. 2IA

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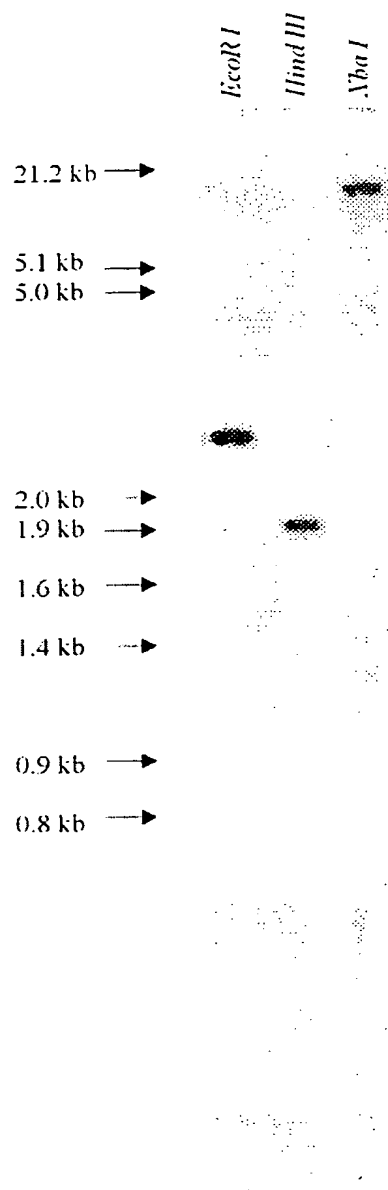


Fig. 22 A



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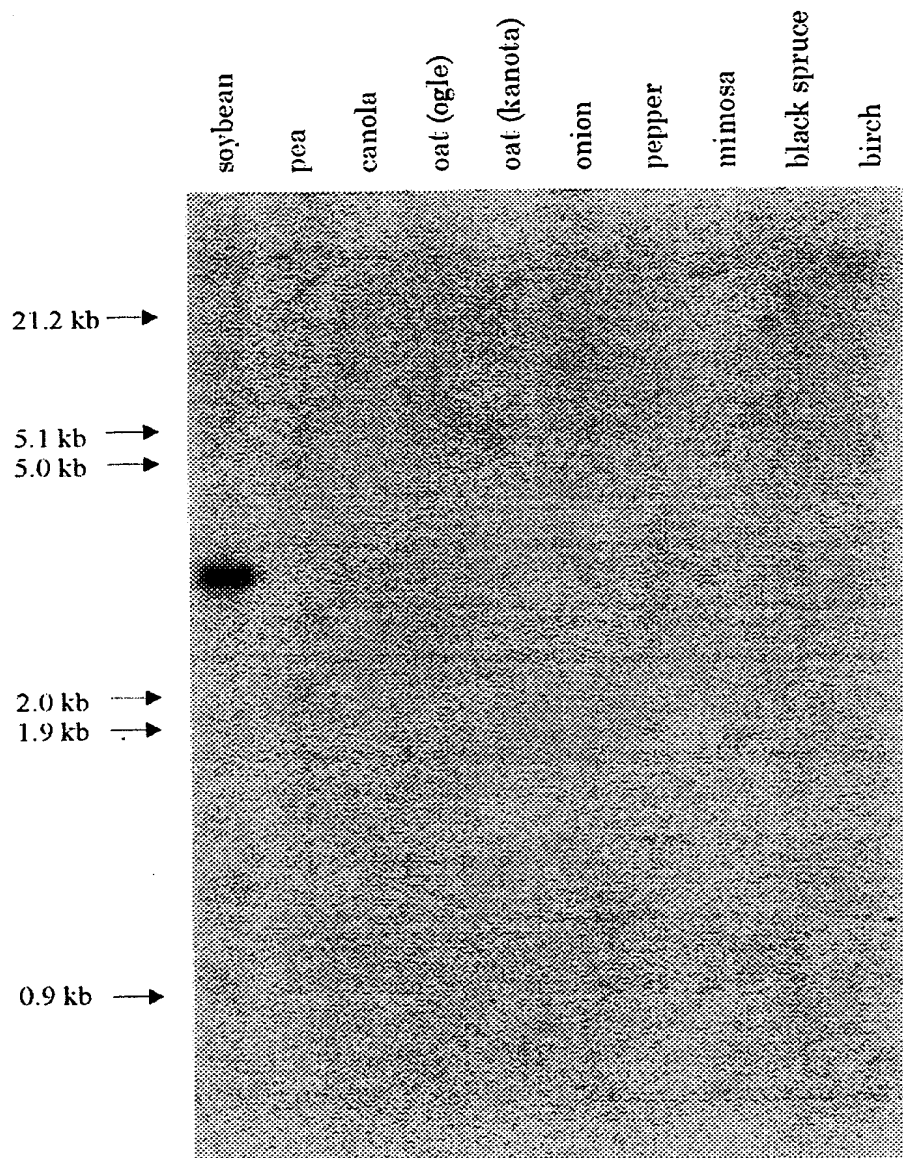


Fig. 22 B

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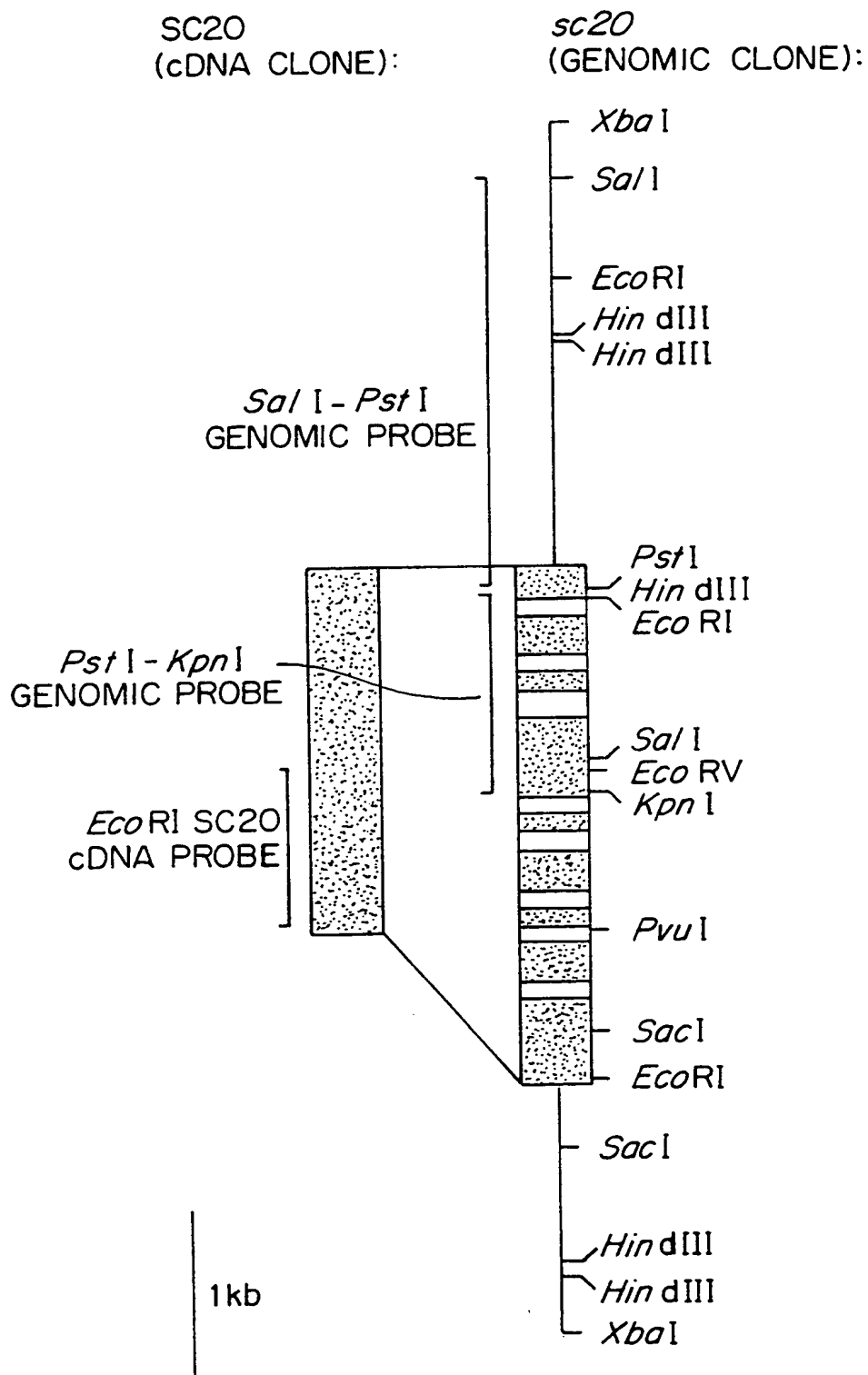


FIG. 23A

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caaagtttttaac ATG AAA GGC AAT AAT ACA CTT TTG TTG CAT TTA TTC TAC ACT ACT CTC 60  
 M K G N N T L L L H L F Y T T L 16

TTC CTG TTT CTT GTA GTG TCA AGT TCA TCT TCA ACA GGG AAT GAA AGT AAC GAT GAC 117  
 F L F L V V S S S S S T G N E S N D D 35

ACT AAC AGT AAA GAA GTT TAT ATC GTG TAC ATG GGA GCT GCA GAT TCA ACA AAA GCT 174  
 T N S K E V Y I V Y M G A A D S T K A 54

TCT CTT AAA AAT GAG CAC GCT CAG ATT CTG AAT TCA GTG CTA AGA AGG AAT GAG AAT 231  
 S L K N E H A Q I L N S V L R R N E N 73

GCC CTA GTA CGG AAC TAC AAG CAT GGT TTC TCT GGG TTC GCA GCT CGT CTA TCA AAA 298  
 A L V R N Y K H G F S G F A A R L S K 92

GAG GAG GCA AAC TCA ATT GCT CAG AAA CCT GGT GTG GTG TCT GTT TTC CCT GAC CCC 345  
 E E A N S I A Q K P G V V S V F P D P 111

ATT CTG AAG CTC CAC ACT ACA CGT TCA TGG GAT TTC CTC AAA AGC CAA ACT CGT GTC 402  
 I L K L H T T R S W D F L K S Q T R V 130

AAT ATC GAC ACC AAA CCA AAT ACG CTG TCC GGT TCT TCT TTT TCT TCA TCA GAC GTC 459  
 N I D T K P N T L S G S S F S S S D V 149

ATT CTT GGC GTC TTA GAC ACA GGC ATA TGG CCA GAG GCG GCG AGT TTT AGC GAC AAG 516  
 I L G V L D T G I W P E A A S F S D K 168

GGT TTC GGT CCT GTT CCA TCC CGA TGG AAA GGC ACC TGC ATG ACA TCA AAA GAC TTC 573  
 G F G P V P S R W K G T C M T S K D F 187

AAT TCC TCT TGT TGT AAC AGG AAG ATA ATT GGC GCG AGG TTT TAC CCT AAC CCA GAG 630  
N S S C C N R K I I G A R F Y P N P E 206

GAG AAA ACG GCA AGG GAT TTC AAC GGA CAT GGG ACT CAC GTT TCG TCG ACG GCA GTG 687  
 E K T A R D F N G H G T H V S S T A V 225

GGC GTG CCG GTG AGT GGC GCA TCG TTC TAT GGT CTG GCG GCG GGG ACG GCA AGG GGT 744  
 G V P V S G A S F Y G L A A G T A R G 244

GGG TCC CCT GAG TCA AGG TTG GCG GTT TAC AAA GTG TGT GGG GCT TTT GGG TCA TGT 801  
 G S P E S R L A V Y K V C G A F G S C 263

CCT GGG TCG GCC ATT CTT GCG GGG TTT GAC GAT GCC ATT CAC GAC GGA GTG GAT ATC 858  
 P G S A I L A G F D D A I H D G V D I 282

TTG TCG CTG TCG CTC GGT GGA TTC GGT GGA ACC AAA ACC GAT TTG ACC ACC GAC CCG 915  
 L S L S L G G F G G T K T D L T T D P 301

ATT GCG ATT GGA GCA TTC CAC TCC GTC CAG CGC GGC ATC CTG GTG GTC TGC GCC GCC 972  
 I A I G A F H S V Q R G I L V V C A A 320

GGG AAC GAC GGA GAA CCA TTC ACC GTT CTC AAC GAC GCA CCT TGG ATT TTA ACC GTT 1029  
 G N D G E P F T V L N D A P W I L T V 339

GCA GCT TCC ACC ATC GAC CGT GAT CTT CAA TCC GAC GTG GTC TTG GGT AAT AAC CAA 1086  
 A A S T I D R D L Q S D V V L G N N Q 358

FIG. 23(B)

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GTC GTC AAG GGA AGA GCC ATA AAT TTC TCC CCT CTT TTA AAT TCT CCC GAT TAT CCA 1143  
 V V K G R A I N F S P L L N S P D Y P 377  
 ATG ATA TAT GCT GAG TCT GCT GCC AGG GCA AAT ATC TCC AAC ATA ACT GAT GCA AGA 1200  
 M I Y A E S A A R A N I S N I T D A R 396  
 CAA TGC CAC CCA GAT TCA TTA GAT CCA AAA AAA GTC ATA GGG AAG ATT GTG GTT TGT 1257  
 Q C H P D S L D P K K V I G K I V V C 415  
 GAT GGA AAA AAT GAC ATT TAT TAT TCA ACT GAT GAG AAA ATT GTC ATA GTG AAG GCG 1314  
 D G K N D I Y Y S T D E K I V I V K A 434  
 TTG GGA GGA ATA GGT CTG GTT CAT ATT ACT GAT CAA TCT GGA TCA GTA GCA TTT TAT 1371  
 L G G I G L V H I T D Q S G S V A F Y 453  
 TAT GTG GAC TTC CCA GTA ACA GAG GTA AAA TCA AAA CAT GGC GAC GCA ATC CTC CAG 1428  
 Y V D F P V T E V K S K H G D A I L Q 472  
 TAC ATC AAC TCA ACT AGC CAT CCA GTG GGA ACA ATA CTA GCA ACA GTT ACA ATT CCT 1485  
 Y I N S T S H P V G T I L A T V T I P 491  
 GAT TAT AAG CCT GCT CCC CGG GTG GGT TAT TTT TCA TCA AGA GGG CCT TCA TTG ATT 1542  
 D Y K P A P R V G Y F S S R G P S L I 510  
 ACA AGC AAT GTT CTC AAG CCT GAT ATT GCA GCC CCG GGA GTT AAC ATT CTC GCT GCA 1599  
 T S N V L K P D I A A P G V N I L A A 529  
 TGG TTT GGA AAT GAC ACA TCA GAG GTT CCA AAA GGA AGA AAG CCC TCA CTA TAT CGC 1656  
 W F G N D T S E V P K G R K P S L Y R 548  
 ATA CTC TCA GGA ACT TCC ATG GCT ACT CCA CAT GTT TCA GGG CTT GCA TGC AGT GTC 1713  
 I L S G T S M A T P H V S G L A C S V 567  
 AAA AGA AAA AAC CCC ACT TGG AGT GCC TCC GCA ATC AAA TCT GCC ATC ATG ACT TCA 1770  
 K R K N P T W S A S A I K S A I M T S 586  
 GCA ATT CAA AAT GAC AAT TTG AAG GGT CCC ATA ACA ACG GAT TCA GGG TTG ATA GCC 1827  
 A I Q N D N L K G P I T T D S G L I A 605  
 ACA CCT TAT GAC TAT GGA GCA GGG GCA ATT ACA ACA TCT GAA CCA TTG CAA CCG GGG 1884  
 T P Y D Y G A G A I T T S E P L Q P G 624  
 CTA GTT TAT GAA ACC AAC AAC GTT GAC TAC TTG AAC TAT TTG TGT TAC AAT GGA CTT 1941  
 L V Y E T N N V D Y L N Y L C Y N G L 643  
 AAC ATA ACC ATG ATA AAG GTC ATC TCC GGA ACT GTC CCC GAG AAT TTC AAT TGT CCC 1998  
N I T M I K V I S G T V P E N F N C P 662  
 AAG GAT TCG AGC TCT GAT CTC ATC TCC AGC ATC AAC TAC CCT TCC ATA GCA GTA AAC 2055  
 K D S S S D L I S S I N Y P S I A V N 681  
 TTC ACT GGC AAA GCA GAC GCG GTC GTG AGT AGA ACT GTC ACA AAC GTT GAC GAA GAA 2112  
E T G K A D A V V S R T V T N V D E E 700  
 GAT GAA ACA GTG TAC TTC CCC GTT GTT GAA GCT CCT AGT GAA GTA ATT GTC ACA CTC 2169  
 D E T V Y F P V V E A P S E V I V T L 719  
 TTT CCA TAT AAT CTT GAG TTT ACG ACA AGT ATT AAA AAA CAA AGC TAC AAT ATT ACT 2226  
 F P Y N L E F T T S I K K Q S Y N I T 739

FIG. 23(B)(Cont'd)

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TTC AGA CCG AAG ACC TCC TTG AAG AAA GAT TTG TTT GGA TCT ATC ACT TGG AGT AAC 2283  
E R P K T S L K K D L F G S I T W S N 757

GAC AAA TAT ATG GTT CGA ATT CCT TTT GTA TTA ACT AAA TAG tgaaattaaaaagtagcga 2344  
D K Y M V R I P F V L T K \* 770

tgaaataaatgcaagctaagttcttcgtgggtgcctacactcgagtcctgattatttattattccatgccttctgt 2419

tttaatttat ttattataact ttcagcct(a)n 2447

FIG. 23(B)(Cont'd)

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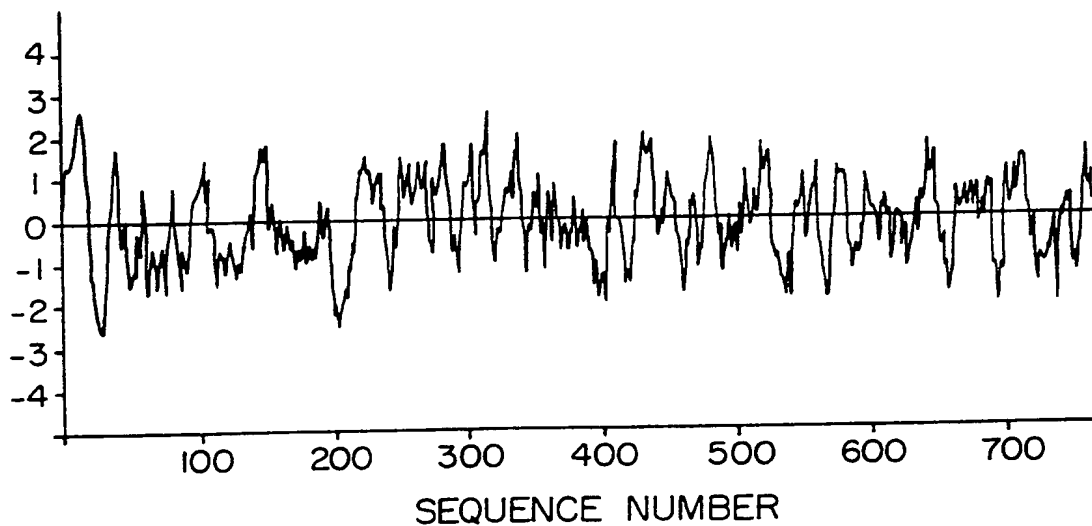


FIG. 23C

FOB220" EEE/960



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## D region

SC20:2  
AF70  
Cucumisin  
P69B  
Agl2  
Subtilisin BPN $\Sigma$   
Kex2  
Furin

\*  
SDVILGVLDGTGI 156  
TDIILGFLDTGI 145  
SNIVVGVLDTGI 143  
KGVIIIGVIDTGI 149  
EDVIIIGVIDSGV 148  
SNVKVAVIDSGI 142  
AGVVAAIVDDGL 178  
HGI VVSILDDGI 156

## H region

SC20:2  
AF70  
Cucumisin  
P69B  
Agl2  
Subtilisin BPN $\Sigma$   
Kex2  
Furin

\*  
DFNGHGTHVSSTAVG 224  
DYQGHGTYTAATAAG 229  
DNTGHGHTTASTAAG 214  
DDIGHGHTTASTAAG 213  
DTLGHGHTTASTAAG 216  
DNNSHGTHVAGTVAA 181  
SDDYHGTRCAGEIAA 223  
NDNRHGTRCAGEVAA 204

## S region

SC20:2  
AF70  
Cucumisin  
P69B  
Agl2  
Subtilisin BPN $\Sigma$   
Kex2  
Furin

\*  
SGTSMATPHVSGLA 562  
SGTSVAVPHVTGAA 571  
SGTSMSCPHITGIA 535  
SGTSMSCPHLSGVA 541  
SGTSMACPHASGVA 547  
NGTSMASPHVAGAA 338  
GGTSAAAPLAAGVY 395  
TGTSASAPLAAGII 378

## N region

SC20:2  
AF70  
Cucumisin  
P69B  
Agl2  
Subtilisin BPN $\Sigma$   
Kex2  
Furin

#  
SVQRGILVVCAAGNDG 322  
ATQKGILVVSSAGNEG 329  
AVERGILTSNSAGNGG 310  
ATERGILVSCSAGNSG 308  
AMEKGVVVSTSAGNAG 318  
AVASGVVVVAAAGNEG 264  
RDSKGAIYVFASGNGG 316  
RGGLGSIFVWASGNGG 297

FIG. 23(D)

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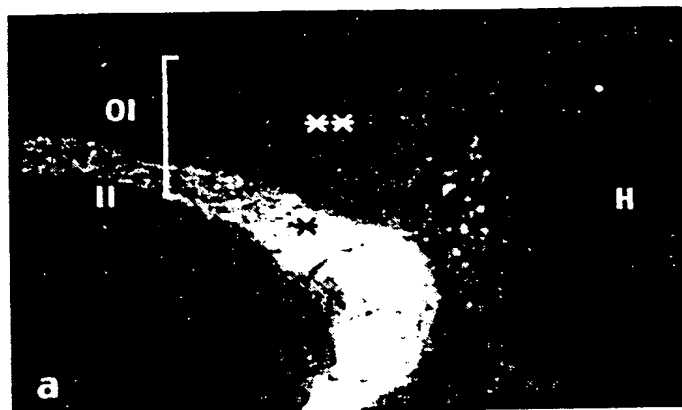


FIG. 24A

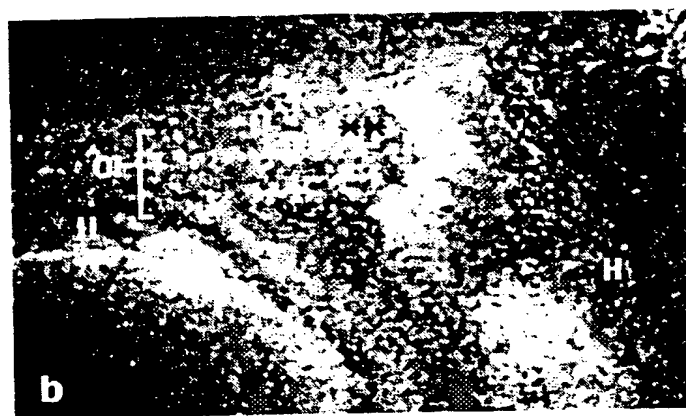


FIG. 24B

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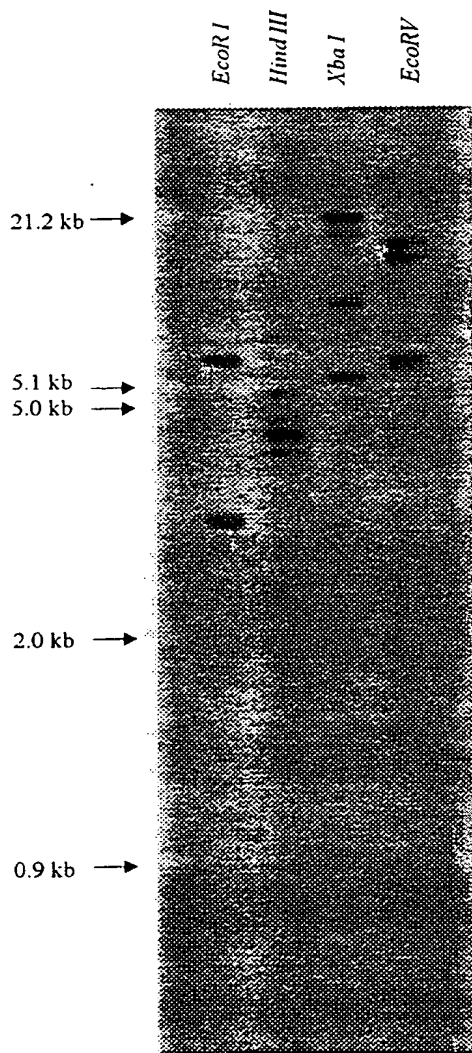


Fig. 25 A



Fig. 25 B

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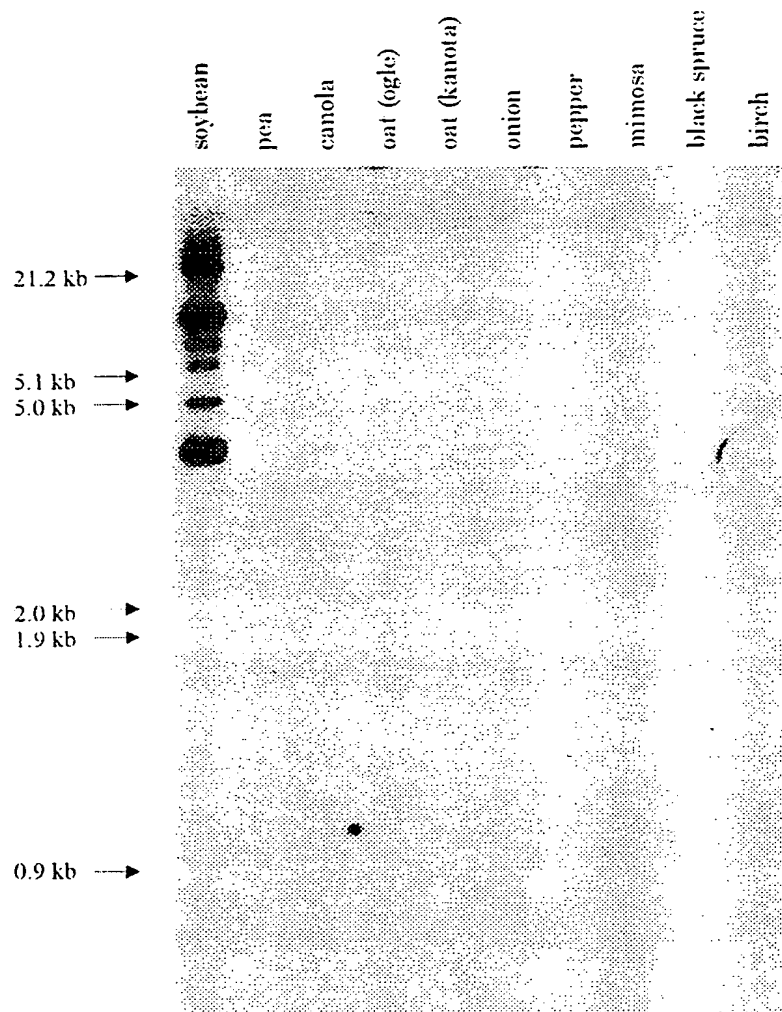


Fig. 25 C